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Result
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Maximum Match 100%
Listing first 45 summaries
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aximum DB seq
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                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length
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ALIGNMENTS

JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS TITLE SOURCE ORGANISM RESULT 1 AC091612/c LOCUS COMMENT DEFINITION KEYWORDS ACCESSION VERSION TITLE JOURNAL Submitted (09-MAY-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Feb 5, 2002 this sequence version replaced gi:15487406. ACO91612

ACO91612

HOMO Sapiens chromosome 1 clone RP11-656022, WORKING DRAFT SEQUENCE, 1 unordered pieces.

ACO91612 AL390860

ACO91612.4 GI:18497169

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Eukaryota; Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 180657)
Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D. Haugen, E.D. Direct Submission Direct Submission Unpublished 2 (bases 1 to 10) 2 (bases 1 to 180657)
Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J., Ivey,R.G. and Homo sapiens

Genome Center

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BASE COUNT
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Contact: uwgchtgs@u.washington.edu
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Location/Qualifiers
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/db_xref="taxon:9606"
/chromosome="1"
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34237 c 35512 g 58545 t
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/clone_lib="RPCI human BAC library
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Homo sapiens chromosome 1 clone RP11-109C14, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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AC026038
AC026038.4 GI:9958133
Direct Submission Submitted (19-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA On Sep 1, 2000 this sequence version replaced gi:8567954.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 138591)
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                                                                            Center code: WUGSC
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Insert size: 140000; agarose-fp Insert size: 136491; sum-of-contigs

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Quality coverage: 3.88 in Q20 bases; agarose-fp Quality coverage: 4.04 in Q20 bases; sum-of-contigs
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Consensus quality: 129539 bases at least Q40
Consensus quality: 131919 bases at least Q30
Consensus quality: 133309 bases at least Q20
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                                                                            accatgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttg
                                                                                                                        CTGACACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGG
                                                                                                                                       ctgacactggctgttgtggacatcatctgcacaacaagcatcataccgaagatgctgggg
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TTCACATGGTCTCTGGGAGCTGAGATGGTTCTCTTCACCACCATGGCCTATGACCGCTAT
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135529. .138591

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1 a 25199 c 25318 g 41754 t 7
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99789. .122864
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126721. .128799
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Pred. No. 3.4e-29
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3.4e-251;
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FEATURES

Location/Qualifiers

/organism="Homo sapiens" /db_xref="taxon:9606"

124905 126621 126721 128800 128900 130562 130662 132548 132648 135429

gap of unknown contig of 1886 gap of unknown

bp in i length

bp in l

of

gd

'n

length bp in .

f unknown
g of 2079
f unknown
g of 1662

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length length

unknown of 1716 unknown of 1840

length

122865 122965 124805 99789 80868 80868

59467 61314

gap of contig

f unknown g of 9828 f unknown g of 1847

length

24124 28989 29089 34172 34272 40990 41090 48356 48456

gap of contig

f unknown
g of 5083
f unknown
g of 6718
f unknown
f unknown
g of 7266

bp in pp in length bp in bp in length

length Length

bp in la length

gap of contig

unknown length of 10911 bp in

9672 13674 13774 13772 18722

gap of contig

length

f unknown g of 4865 f unknown g of 5202 5321: 9571: 9671:

of 5221 unknown

bp in

Length

contig of 4250 gap of unknown contig of 4002 less gap of unknown contig of 4948 less conting of 4948 less contig of 4948 less contig of 4948 less conting of 494

source

misc_feature

vector_side:left"
5322. .9571 clone_end:T7

/note="assembly_name:Contig10

/note="assembly_name:Contig11"

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sum-of-contigs Quality

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Homo sapiens chromosome 1 clone RP11-634B7,
PROGRESS ***, 18 unordered pieces.
Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 183408 bases at least Q40
                                                                                     Center project name: bA634B7
                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                       Center: Sanger Centre
Center code: SC
                                                                                                                                                                                                                          requests: clonerequest@sanger.ac.uk
on Aug 12, 2000 this sequence version
                                                                                                                                                                                                                                                                Submitted (18-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                              (bases 1 to 190889)
                                                                                                                                                       site:
                                                                                                                                                       http://www.sanger.ac.uk
                                                                             Summary Statistics
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12042: contig of 12042 bp in length
12043 12142: gap of 100 bp
12143 30362: contig of 18120 bp in length
12043 130362: contig of 18120 bp in length
130263 30362: gap of 100 bp
14126 41525: gap of 100 bp
141526 48351: contig of 6826 bp in length
141526 48451: gap of 100 bp
148452 48451: gap of 100 bp
157809 57908: gap of 100 bp in length
16844 68743: gap of 100 bp
16844 68743: gap of 100 bp
16874 75536: gap of 100 bp
16874 75536: gap of 100 bp
175637 884190: contig of 8793 bp in length
175637 884290: gap of 100 bp
17667 884291 89039: contig of 8793 bp in length
17667 884291 89039: contig of 87449 bp in length
180040 80139: contig of 4749 bp in length
180040 80139: contig of 4749 bp in length
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106021 133564: contig of 27544 bp in length
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174410 174509:
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                                                                                                                                                                       fragment
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fragment_chain:1
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                                                       /note="assembly_fragment:00297
fragment_chain:2"
                     /note="assembly_fragment:00082
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190889: contig of 16380 bp in length
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159175; contig of 15562 bp in length
59275; gap of 100 bp
174409; contig of 15134 bp in length
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105920: contig of 11304 bp in length
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Matches 922; Conservative
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174510. .190889
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133665. .137940
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143614. .159175
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159276. .174409
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Bellenson, J., Smith,
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/db_xref="taxon:32630"
/note="(H389459 nucleotide)"
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l (sites)
Shendy,S., Gangolli,E.A., Rastelli,L., Smithson,G., Padis Shenty,S., Gangolli,E.A., Casman,S.J., Tchernev,V.T., Vernet,C.A., Wolenc,A.R., Casman,S.J., Tchernev,V.T., Szekeres,E.S., Gorsse,W., Alsobrook,J.P. and Burgess,C.E. Novel gpcr-proteins and nucleic acids encoding same
                              Homo sapiens
Eukaryota; M
                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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                          Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bouslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Dastien, V., Bouslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Callins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Gollins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Galagan, J., Gardyna, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., LaRocque, K., Lu, G., Maclean, C., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marpqis, N., Meldrim, J., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Jahnoun, J., Zembek, L., Zinmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum, Mus musculus, clone RP23-240K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                         Summary Statistics
Sequencing vector: plasmid; 'n/a; 100% of reads
Sequencing vector: plasmid; 'n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 221031 bases at least 040
Consensus quality: 221147 bases at least 030
Consensus quality: 221146 bases at least 020
Insert size: 230000; agarose-fp
Insert size: 231266; sum-of-contigs
Quality coverage: 11.4 in 020 bases; sum-of-contigs
Quality coverage: 11.9 in 020 bases; sum-of-contigs
                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                     as soon as it is available and the be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
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1 9911: contig of 9911 bp
9912 10011: gap of 100 bp
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Eutheria; Rodentia;
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Rattus norvegicus clone CH230-5M10,
65 unordered pieces.
AC094718
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Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Weinstock,G. and Gibbs,R.
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IN PROGRESS ***,
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Barbaria,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
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Consensus quality: 137458 bases at least Q30
Consensus quality: 144882 bases at least Q30
consensus quality: 144882 bases at least Q20
Estimated insert size: 129461; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estim
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80018 80018 gap of unknown length
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80019 80348 gapt of unknown length
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	780 12800	Oy 721 catctcacagtggtgaccctttactattctcctgtaatctacacctatatccgccctgct	
	720 12860	Qy 661 gctattctccgtatccgcacagtagaaggcaagaggaaggccttctcaacatgctcatct	
	660 12920	Qy 601 attaccotggccataggggactttattcttacctgcatctcctatggttttatcattgtt	
	600 12980	Qy 541 ttgctggctttgtcctgtagccctgtaagaatcaatgaggtgatggtgtatgttgctgatgt	
	540 13040	Qy 481 atgaggttgactttctgtgggccaaacaccattgaccacttcttctgtgagataccccca	
	480 13100	Qy 421 ttgctcagcatggtcatggctattgcagtcaccaattcctgggtgcacacagctcttatc	
	420 13160	Oy 361 gtggccatttgtttccctcttcattacagtactattatgaaccaccatatgtgtgtagcc	
	360 13220	Qy 301 ttcacatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctat	
	300 13280	Oy 241 accatgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttg	
	240 13340	Oy 181 ctgacactggctgttgtggacatcatctgcacaacaagcatcataccgaagatgctgggg	
	180 13400	OY 121 ctcatcattcattgccaaaatctatagcaacaccttgcatacgcccatgtatgt	
	120 13460	Oy 61 cagggaattatottoctottttttotcattgtotatottgtggottttotcgggaascatg	
	60 13520	Oy 1 atgaatcacagcgttgtaactgagttcattattctgggcctcaccaaaaagcctgaactc	
0;	aps	Query Match 72.1%; Score 666.6; DB 2; Length 160483; Best Local Similarity 82.6%; Pred. No. 9.8e-179; Matches 762; Conservative 0; Mismatches 161; Indels 0; G	
		* 147478 148718: contig of 1241 bp in length * 148719 148818: gap of unknown length	

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                                                                                               ttcacatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctat
                                                                                                                                                                                                                     atgaggttgactttctgtgggccaaacaccattgaccacttc-ttctgtgagata-cccc
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 926)
Zhang, X. and Firestein, S.
The olfactory receptor gene superfamily of the mouse nat. Neurosci. 5 (2), 124-133 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
AY073900
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Mus musculus olfactory receptor
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                                                                                                                                                                                                                                                                                                                        Conservative
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/db_xref="taxon:10090"
/chromosome="7"
<1. .>926
                                                                                                                                                                                                                                                                                                                                                                                                      /gene="olfactory receptor MOR251-4P"
/note="potential coding region disrupted
internal stop codons"
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/evidence=not_experimental
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Pred. No. 1.1e-178;
0; Mismatches 144;
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AAGTATTTGCATTTTTAAAA 923
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Sequence
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AX350675.
                                                                                                                                                                                                 Shenoy, S., Gangolli, E.A., Rastelli, L., Smithson, G., Padig Vernet, C.A., Wolenc, A.R., Casman, S.J., Tchernev, V.T., Szekeres, E.S., Gorsse, W., Alsobrook, J.P. and Burgess, C.E. Novel spcr-proteins and nucleic acids encoding same Patent: WO 0177177-A 53 18-OCT-2001;
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                             Curagen
                                                                                                                                                                                                                                                                             human
                                                                                                           Similarity
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                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
174 c 134 g 20
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                              GI:18616221
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                                                                                                           71.6%;
                                                                                                    Score 661.4; DB 6; Pred. No. 1.7e-177; 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                               663 bp
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                                                                   Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gaqe, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N., Halme, S., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehorsky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacLean, C., Macdonald, P., Major, J., Marquis, N., Meldrim, J., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McCarthy, M., McDan, P., McKernan, K., McPheeters, R., Meldrim, J., McDub, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Norman, J., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Rogetti, M., Ribe, R., Schauer, S., Schuber, R., Rogetti, M., Roye, A., Santos, R., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, R., Rogetti, M., Roye, A., Santos, R., Schauer, S., Scha
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Aller Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhg. Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, E., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P.
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Mus musculus, clone RP23-101J20
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Birren, B., Linton, L.,
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Mus musculus clone RP23
AC101272
AC101272.1 GI:17060047
                             Roman, J., Rosetti, M., Seaman, S., Severy, P.,
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                      Roy, A., Santos, R., Schauer, S., Schupback, R., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
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Research, 320 Charles Street, Cambridge, MA 02141,
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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----- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         will be sequenced to completion. In the event th
the record is updated, the accession number will
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Zhang, X. and Firestein, S.
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                                                                                                                                                                                                                                                   Submitted (11-JAN-2002) Celera Rockville, MD 20850, USA
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RRS Muzny,D.M., Adams,C., Addo-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Balsbrooks,S.L., Amaratunge,H.C., Are,J.R., Bonin,D., Bouck,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Burbaria,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Burbaria,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Burbaria,J., Bouck,J., Binage,K., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Bowie,S., Brieva,M., Bryant,N.P., Buhay,C., Carton,T.F., Carton,P., Charke,C., Chen,G., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC094870 112730 bp 1
Rattus norvegicus clone CH230-5N18,
52 unordered pieces.
AC094870 GI:17941654
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                  Submitted (15-SEP-2001) Human Genome Sequencing Center, Depar
of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624706.
                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Center project name: GBPG
Center clone name: CH230-5N18
------ Summary Statistics
                                                                                              Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                  Center: Baylor College of Medicine
                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                          Center code:
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Assembly program: Phrap; version 0.990329First call findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edv/docs//Genbank_draft_data.html).
NOTE: This is a 'working draff' sequence. It currently consists of 52 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 96697 bases at least Q40 Consensus quality: 104847 bases at least Q30 Consensus quality: 112411 bases at least Q20 Estimated insert size: 92352; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 1.1x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttgctcagcatggtcattgcagtcaccaattcctgggtgcacacagctcttatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtggccatttgtttccctcttcattacagtactattatgaaccaccatatgtgtgtagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCACATGGTCCATGGGGGCAGAGCTTCTGCTCTTCTCAGCTATGGCTTATGACCGCTTC 95988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttcacatggtctctgggagctgagatggttctctttcaccaccatggcctatgaccgctat 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCATGGT---AGGGGGAAGGACCATCTCTTATGGTGGCTGCATGGCCCAGCTCTTCTTC 96048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gctattctccgtatccgcacagtagaaggcaagaggaaggccttctcaaccatgctcatct 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTTTCTGGCTGTAGGGAACTTCTCTGTGATCATCCTCTCCTATGGCTTTATTGTGACC 95688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTTGAACCCCCTCATCTACACTCTGAGGAACAAAGATGTCAAAGTTGCACTCCGGAA 95449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acattaaaccogatggtgtacagcttccagaatagggagatgcaggcaggaattaggaa 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tccagctatacatttgaaagagacaaggtggtagctgcactctatactcttgtgactccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              catotoacagtggtgaccotttactattotcotgtaatctacacotatatcogcoctgct 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCAGCTACTCATTGAACAAGGACAAGGTGGTGTCCATCATCTACACTTCGGTGGCACCC
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J. Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Burch,P., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davila,M.L., Dav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 unordered pieces.
AC094700
AC094700.4 GI:17941479
HTG; HTGS_PHASE1.
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Rattus norvegicus clone CH230-5F7,
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Norway rat.
                                                                                                                                                                                                                                                                                                                Rattus.
                                                                                                                                                                                                                                                                                      (bases 1 to 197438)
                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
SEQUENCING
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N PROGRESS ***,
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Dugan-Rocha, S. Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harth, M., Havlak, P., Hawes, A., Heminandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lozado, R.J., Lu, X., Lucker, A., Lucker, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Okumon, G., Oragunye, N., Nickeson, E., Newkson, N., Nuckerson, E., Payton, B., Oguine, M., Okumon, G., Oragunye, N., Oviedo, R., Payton, B., Ouiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Payton, B., Stone, H., Sutton, A., Syatek, A., Tabor, P., Tamerisa, N., Tamerisa, K., Tamarisa, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward, More, G., Willamson, A., Wleczyk, R., Wooden, S., Walliams, G., Willamson, A., Wleczyk, R., Wooden, S., Walliams, G., Willamson, A., Wleczyk, R., Wooden, S., Weinstolm, R., Wang, S., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Vinson, R., Pare, S., Stan, S., Stan, R., Pare, S., M., Rock, R., Payton, C., Wallans, A., Wleczyk, R., Wooden, S., Weinstole, R., Wang, S., Wallans, A., Wleczyk, R., Wooden, S., Weinstole, R., Wang, S., Wallans, A., When, S., Wallans, A., Wallans, A., Wallans, A., Wallans, C., Wallans, A., Wallans, A., Wallans, A., Wallans, A., Wallans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Denn, A.L., Ding, Y., Dinh, H.H., Dugan-Rocha, S., Durbin, K.J., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-SEP-2001) Human Genome Sequencing Center, Departure of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17062158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                              * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 96 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                        as soon as it is available and the be preserved.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: Phrap; version 0.990329First call
                                           6381
6481
11236
11336
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6480:
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): contig of 6380 bp in length
): gap of unknown length
): contig of 4755 bp in length
): gap of unknown length
]: contig of 2747 bp in length
]: gap of unknown length
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                                                                                                                                                                                                                                                                                                 accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draper, H.,
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Оу	Qу Дъ	Оу	Qy	Qy Db	Qу	Qy Db	Qy	Дy	Z # O	
481 atgaggttgactttctgtggggccaaacaccattgaccacttcttctgtgagataccccca 540	421 ttgctcagcatggtcatggctattgcagtcaccaattcctgggtgcacacagctcttatc 480	361 giggocattigiticocitoticattacagiactattatgaaccaccatatgigigiagoc 420 	301 ttcacatggtctctgggagctgagatggttctctttcaccaccatggcctatgaccgctat 360	241 accatgctaacatcagaagaataccatttcatatgcaggctgcatgtcccagctcttcttg 300	181 ctgacactggctgttgtggacatcatctgcacaacaagcatcataccgaagatgctgggg 240	121 ctcatcattgccaaaatctatagcaacaccttgcatacgcccatgtatgt	61 cagggaattatetteetettttteteattgtetatettgtggetttteteggeaacatg 120	1 atgaatcacagcgttgtaactgagttcattattctgggcctcaccaaaaagcctgaactc 60	Query Match 36.7%; Score 339; DB 2; Length 197438; Best Local Similarity 62.6%; Pred. No. 2.3e-85; Matches 563; Conservative 0; Mismatches 330; Indels 6; Gaps 2;	# 110131 110230: gap of unknown length # 111401 111500: gap of unknown length # 111501 113819: contig of 1170 bp in length # 113820 113919: gap of unknown length # 113920 115967: contig of 2018 bp in length # 11506 115067: gap of unknown length # 117165 117164: contig of 1097 bp in length # 117165 117264: gap of unknown length # 117165 118813: contig of 1670 bp in length # 118914 118913: gap of unknown length # 120584 120583: contig of 1670 bp in length # 122742: contig of 2058 bp in length # 122742: contig of 2058 bp in length # 122742: contig of 2058 bp in length # 122705 125204: gap of unknown length # 127019 128590: contig of 1814 bp in length # 128591 128690: gap of unknown length # 128691 129819: contig of 1472 bp in length # 129820 129919: gap of unknown length # 131057 131156: gap of unknown length # 131059 135188: contig of 1874 bp in length # 131059 135188: contig of 1874 bp in length # 136714 138549: contig of 1874 bp in length # 136714 138549: contig of 1874 bp in length # 136714 138549: contig of 1874 bp in length # 136714 138549: contig of 1874 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138549: contig of 1876 bp in length # 136714 138550 138649: gap of unknown length # 136714 138550 138649: gap of unknown length # 136714 138550 138649: gap of unknown length # 136714 138549: contig of 1876 bp in length # 136714 136715 136715 136715 136715 136715 136715 136715 136715 136715 136715 136715 136715 136715 136715 136715 1367

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DEFINITION
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                                                                                                                 Rattus.

CE 1 (bases 1 to 204143)

CE 1 (bases 1 to 204143)

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

RS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

RS Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Bonnin,D., Bouck,J.,

Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Bowie,S., Brieva,M., Brown,E., Brown,D., Charco,T.F.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Chen,G., Ch
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                         Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
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Sutton, A., Svatek, A., Tabor, P.,
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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                  Tamerisa, A.,
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                     Tamerisa, K.
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Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
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Direct Submission
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 62 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Consensus quality: 170292 bases at least Q30
Consensus quality: 181161 bases at least Q20
Consensus quality: 181161 bases at least Q20
Estimated insert size: 177160; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
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	* 190645 190744: gap of unknown length * 190745 191885: contig of 1141 bp in length * 191886 191885: gap of unknown length * 19188 193129: contig of 1144 bp in length * 193130 193229: gap of unknown length * 193230 194840: contig of 1611 bp in length * 194841 194940: gap of unknown length * 194941 196463: contig of 1523 bp in length * 196464 196563: gap of unknown length
<u> </u>	Query Match 35.8%; Score 331.2; DB 2; Length 204143; Best Local Similarity 60.0%; Pred. No. 3.9e-83; Matches 552; Conservative 0; Mismatches 368; Indels 0; Gaps 0;
	QY 4 aatcacagcgttgtaactgagttcattattctgggcctcaccaaaaagcctgaactccag 63
	Qy 64 ggaattatcttcctcttttttctcattgtctatctttgtgggcttttctcgggcaacatggtc 123
	QY 124 atcatcattgccaaaatctatagcaacaccttgcatacgcccatgtatgt
	QY 184 acactggctgttgtggacatcatctgcacaacaagcatcataccgaagatgctggggacc 243
	QY 244 atgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttgttc 303
	Qy 304 acatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctatgtg 363
	Qy 364 gccatttgtttccctcttcattacagtactattatgaaccaccatatgtgtgtagccttg 423
	Qy 424 ctcagcatggtcatggctattgcagtcaccaattcctgggtgcacacgctcttatcatg 483
	Qy 484 aggttgactttctgtgggccaaacaccattgaccacttcttctgtgagatacccccattg 543
	QY 544 ctggctttgtcctgtagccctgtaagaatcaatgaggtgatggtggtgtatgttgctgatatt 603
	Qy 604 accetggccataggggactttattettacetgcatetectatggttttatcattgttgct 663
	Qy 664 attotccgtatccgcacagtagaaggcaagaggaaggccttotcaacatgctcatctcat
	Qy 724 ctcacagtggtgaccotttactattctcctgtaatctacacctatatccgccctgcttcc 783
	Qy 784 agctatacatttgaaagagacaaggtggtagctgcactctatactcttgtgactcccaca 843
	Qy 844 ttaaacccgatggtgtacagcttccagaatagggagatgcaggcag

59276 CTCAACCCTCTGATCTACACTTTGAGAAACAAGGAGGTCAAGGCAGCTCTCAGGAAAATT 59335

Qy 904 tttgcatttctgaaacacta 923
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Db 59336 TTCCCTTTTCTCAGAAATTA 59355

Search completed: June 21, 2002, 12:36:47
Job time: 8112 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The which encode polypeptides can be used in screening for olfactory agonists and polynucleotides can be used in screening for olfactory agonists and tagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. The receptors that are involved in detecting such secondary scents as scent fingerprint or scent profile), which may be used to re-create a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for and edit scents. Libraries of olfactory receptors are useful for the receptor of the profile of the scent profile of the sce
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treatment of e.g. cardiomyopathy, a
modulators -
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The invention relates to Human G-protein coupled receptor (GPC polypeptides, designated NOV1-12, nucleic acids encoding them, variants of them, a vector containing the nucleic acid, a host containing the vector, a method for identifying modulators of

(GPCR) host

of the

GPCRs

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cc and antibodies raised against them. The NOVI-12 polypeptides and nucleic cc acids are used to identify ligands and ant/agonists, they are also used cc to diagnose and treat GPCR-associated diseases, e.g. cardiomyopathy, cc atherosclerosis, diseases related to cell-signalling or metabolic catherosclerosis, diseases related to reprotozoal infections, pain, cc pathways, bacterial, viral, fungal or protozoal infections, pain, cc Alzheimer's diseases) stroke, multiple sclerosis, lesional cc psoriatic skin, ischaemia, cirrhotic hepatitis, acute pancreatitis, cd disbetes, cancer, anglogenesis, obesity, also disorders of olfactory cf function. The nucleic acids can be used as marker for chromosome 11, cc therapeutically, including as antisense or ribozyme sequences, to prepare transgenic animals, as sources of primers and probes (e.g. for transgenic animals, as sources of primers and probes (e.g. for therapy, and for tissue typing. The present sequence encodes human NoV6.
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26-MAY-2000;
23-JUN-2000;
16-AUG-2000;
07-SEP-2000;
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                                                                                           The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific specificatory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds encoding them are useful for paramacoustic modulations of their activity are useful for pharmacoustal and genetic modulation of their activity are useful for pharmacoustal and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, olfactory signalling pathways inherefore, they can be dours and pharmaceutical and cosmetic industries to customise odours and fragrances. The present sequence encodes a human olfactory receptor of
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P-PSDB; AAU24591.
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537; Conserv
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Human; G-protein coupled receptor-9; GCREC-9; cytostatic; hepatotropic;
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virucide; antiinflammatory; anticonvulsant; antiemetic; neuroprotective; nootropic; cerebroprotective; hypotensive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; Huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia; anorexia; gastrointestinal disorder; panoreatitis; autoimmune disorder; haddison's disease; Crohn's disease; acquired immune deficiency syndrome; hads; uveitis; infection; trauma; metabolic disorder; diabetes; obesity;
osteoporosis;
transgenic animal; gene therapy; ss.
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Homo sapiens

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CDS
                        Location/Qualifiers 255..1241
/*tag=  a
/product= "Human GCREC-9 protein"
              /*tag=
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WO200157085-A2

09-AUG-2001

01-FEB-2001; 2001WO-US03455

02-FEB-2000; 11-FEB-2000; 2000US-0180093. 2000US-0182045.

(INCY-) INCYTE GENOMICS INC

Baughn MR, Au-Young ۲

P-PSDB; 2001-488869/53.

preventing and of cardiovascular, Novel isolated human G-protein coupled receptor useful for diagnosing, treating cell proliferative, neurological, gastrointestinal, autoimmune/inflammatory and metaboli. and metabolic

Claim 5; Page 133; 138pp; English.

CC CDNA. The present sequence is human G-protein coupled receptor-9 (GCREC-9)
CC cDNA. The present invention relates to GCREC protein and nucleic acids
CC colon, The present invention relates to GCREC protein and nucleic acids
CC concerning diseases or conditions associated with decreased expression
CC or overexpression of functional GCREC in a patient, where the disorder
CC is selected from cell proliferative disorders such as actinic keratosis,
CC concer, neurological disorders such as epilepsy, stroke, Alzheimer's
CC disease, Huntington's disease, Parkinson's disease, cardiovascular
CC disease, Huntington's disease, Parkinson's disease, cardiovascular
CC disorders such as hypertension, vasculitis, varicose veins, gastroCC intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea,
CC uveitis, autoimmune/inflammatory disorders such as acquired
CC infections, trauma and metabolic disorders such as diabetes, obesity,
CC osteoporosis. GCREC proteins and their CDNAs are used to assess the
CC effects of exogenous compounds on the expression of GCREC sequences.
CC GCREC CDNA is useful to create knock in humanised animals (pigs) or
CC therapeutic or diagnostic purposes, for somatic or germline gene
CC therapy, to generate hybridisation probes useful in mapping the
CC techniques
CC techniques

Sequence 1241 BP; 259 A; 366 Ç 295 <u>ი</u> 321 ., 0 other;

Query Match
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Matches 537; Conserv Conservative 33.2%; 0, Score 307.2; Pred. No. 4. .9e-85; DB 22; Indels Length 1241; 0 Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds.
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24-FEB-2000; 2000US-0184809
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milarity 58.4%;
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Query Match
Best Local Similarity
Matches 505; Conser

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Score 267.4; Pred. No. 1.1e 0; Mismatches

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                                                     The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors and can be used for determining differences in the olfactory faculties
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotides which encode polypeptides involved in olfactory sation for identifying olfactory agonists and antagonists -
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The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of

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04-JAN-2001;
13-MAR-2001;
  The
                                        G-Protein coupled receptor polypeptides and NAs useful preventing, diagnosing and treating cardiomyopathy, athoracers and diabetes -
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                     Claim 5;
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2000US-275226P.
2000US-256399P.
2000US-25624P.
2000US-258159P.
2000US-258511P.
2000US-25882BP.
2000US-25882BP.
2001US-259659P.
2001US-0275226.
   sequence
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                                                                                                   Burgess CE, Casman Smithson G;
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SJ, Lepley
 coupled
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DM, Gangolli
receptor-17
                                                  atherosclerosis,
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  (GPCR-17)
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treatment of diseases associated with inappropriate GPCRX expression, obesity, diabetes mellitus, anorexia, cachexia, cardiomyopathy, pain, atherosclerosis, neurodegenerative disorders (Alzhelmer's disease, Parkinson's disease, Huntington's disease); bullmia, immune disorder, parkinson's disease, Huntington's disease); bullmia, immune disorder, haematopoletic disorders, disorders related to cell signal processing and metabolic pathway modulation, retinal disorder (photoreception), bacterial, fungal, protozoal and viral infections (HTV); cancer (neopladenocarcinoma); angina pectoris, hypotension, hypertension, asthma, Crohn's disease, multiple sclerosis, ulcers, neurological disorders (dementia, mental retardation, schizophrenia, anxiety); acute heart failure, osteoporosis, myocardial infarction and urinary retention.
                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA. GPCR protein and DNA may treatment of diseases associate
                                                                                                             Sequence 1050 BP;
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Query Match
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Matches 499; Conserv
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RESULT 11
AAA51177
Degenerate primer; ligand-binding region; olfactory receptor; Transmembrane domain; N-terminal; plasma membrane; translocation human rhodopsin receptor; odorant; toxicity; olfactory response;
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                                                        Murine olfactory receptor ligand-binding region cDNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                          transmembrane domains (TMD) II-VI, III-VI, IÎ-VII or III-VII. Chimeric nucleic acids encoding a 7-TMD protein comprise a sequence encoding an N-terminal plasma membrane translocation domain (especially the sequence shown in AAY96658), a first TMD and the OR-LBR. The translocation domain was initially derived from the N-terminus of the human rhodopsin receptor. LBR produced by amplification with the primers are useful for generating new odorants, to screen for toxicity or therapeutic activity in odorants, and altering an animal's olfactory response (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer pair for amplifying olfactory receptor nucleic acid, useful for producing receptor libraries used in e.g. screening odorants for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 encode murine odorant/ligand binding regions of olfactory. They were amplified using degenerate primers shown in
                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                           The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary
                                           receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also c
                                                                                         these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour
                                                                                                                                                                                                                                                                                    Claim
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int or scent profile), which may Libraries of olfactory receptors
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                                             actcaccctgaggacactgataagattggtgctgtcctattcactgtggtgacacccatg
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24-MAR-2000;
12-APR-2000;
24-APR-2000;
26-MAY-2000;
23-UUN-2000;
16-AUG-2000;
07-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific split split split specific split 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human olfactory G protein-coupled receptors, useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customise odours .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 83-84; 319pp; English
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food additive; cosmetic;
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DB; AAU24516
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aacctcctctttgtgcttttcttgggtatgtacctggtcactgtgattgggaacgggctc
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2000US-0230732.
2001US-0266862.
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fragrance; pharmaceutical additive.
                                                                                                                                                                                                                      Score 255.8; DB 22;
Pred. No. 4.4e-69;
Pred. No. 4.4e-69;
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                                                    Human; cytostatic; neuroprotective; immunosuppressant; nootropic; anti-inflammatory; anti-viral; gastrointestinal; cardiovascular; cerebroprotective; G-coupled receptor; cell proliferative disease; lymphoma; leukaemia; breast cancer; cirrhosis; neurological disorder; stroke; Alzheimer's disease; multiple sclerosis; mental retardation; cardiovascular disease; atherosclerosis; angina pectoris; indigestion; congestive heart failure; gastrointestinal disorder; dysphagia; AIDS; gastritis; autoimmune disorder; inflammatory disorder; Crohn's disease; gastritis; autoimmune disorder; inflammatory disorder; Crohn's disease;
           systemic lupus erythematosus; metabolic disorder; viral infection; herpesvirus; parvovirus; acquired immune deficiency syndrome; ss.
                                                                                                                                                                                               Human G-coupled receptor (GCREC) cDNA,
                                                                                                                                                                                                                                  14-MAR-2002
                                                                                                                                                                                                                                                                                              ABK16620 standard;
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02-JUN-2000;
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07-JUN-2000;
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ALIGNMENTS

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APPLICANT: Firestein, Stuart
APPLICANT: Zhao, Haiqing
TITLE OF INVENTION: Functional Expression
TITLE OF INVENTION: Vivo
FILE REFERENCE: P01511USZ / 09805059
CURRENT APPLICATION UNMBER: US/09/085,371
CURRENT FILING DATE: 1998-05-19
PRIOR APPLICATION NUMBER: US 08/891,243
PRIOR APPLICATION NUMBER: US 60/045,961
PRIOR APPLICATION NUMBER: US 60/045,961
PRIOR APPLICATION NUMBER: US 60/045,961
PRIOR FILING DATE: 1997-05-07
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
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                                              ctggagatttggtatgtcactgttacgattcctaagatgctcgctggcttcattggttcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ronnett et al. TITLE OF INVENTION: NOVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604
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                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 cgcctgtcttactgtggccccaacaccatcaaccactttttctgtgatgtgtctccattg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544
                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   688
                                                            ATTORNEY/AGENT INFORMATION:
               REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                STREET: Two Proceed CITY: Chicago STATE: IL
                                                                                                                                                     FILING DATE: 08-NOV-1996
                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                     COUNTRY:
TELEFAX:
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US-08-748-506-7
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SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                  TIGCCTGTGGTGATACATCCCAAAATGAGGCTGCCATCTTTGTGGCAGCAGTGCTCTGCA 637
                                                                                                                                                                                                                                                                                      tgtcctgtagccctgtaagaatcaatgaggtgatggtgtatgttgctgatattaccctgg
                                                                                                     TAGTCACACTCTTCTATGGCTCAACATCTGCCACCTATTTGAGGTCCAAGTCTAGCCACT
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                                                                                                                        tggtgaccetttactatteteetgtaatetacacetatatcegecetgetteeagetata 790
CCATCATCTACAGCTTAAGGAACAAGGAAGTAAAGGGTGCACTGAGAA
              CACCAGGAGTGGACAAACTCTTGGCCCTCTTCTATACATCAGTGACATCCATGCTGAATC
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 Mismatches

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pred. No. 5.3e-50;
0; Mismatches 399;
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RESULT 3 US-08-748-506-8

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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.9%; Score 184; DB 3; Length 966; Best Local Similarity 51.1%; Pred. No. 3.1e-48; Matches 433; Conservative 0; Mismatches 415; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08748506 Patent No. 6159707
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APPLICANT: RONNET et al.

TITLE OF INVENTION: NOVEL SPERM RECEPTORS

NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5500
TELEPAX: 312-616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
458 TTTCATGGGTGATGGGATGCATAGTAGGTCTGGGACAGACCAATTTTATTTTCTCCTTGA
                            431 tggtcatggctattgcagtcaccaattcctgggtgcacacagctcttatcatgaggttga 490
                                                                                                                        371 gtttccctcttcattacagtactattatgaaccaccatatgtgttgttagccttgctcagca 430
                                                                                                                                                                                                           311 ctctgggagctgagatggttctcttcaccaccatggcctatgaccgctatgtggccattt 370
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                                                                                                                                                                                                                                                                                                                                                                  218 CTCTCCTGGAGATTGGCTATACTTGCTCTGTCATACCCAAGATGCTGCAGAGTCTTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 TTGCTATTTGTACCAGTCCATCTCTACACACCCCCCATGTACTTCTTCTTGGCCAACTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 TGTTCACCCTCATCCTTCTCATGTTCTTAGTATCACTAACAGGAAATGCTCTCATAGCCC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 tetteetetttttteteattgtetatettgtggetttteteggeaacatgeteatea 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
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US-08-748-506-5

Query Match
Best Local Simi
Matches 424;

Local Similarity

19.8%;

Score 182.8; DB 3; pred. No. 7.4e-48;

Length

966; 0;

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Mismatches 404; Indels

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71 tetteetetttttteteattgtetatettgtggetttteteggeaacatgeteateatea 130

TGTTCAACCTCATCCTTCTCATGTTCTTAGTATCACTAACAGGAAATACTCTCATAGTCC 157

Beecham Corporation

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Sequence 1, Application US/08827291A
Patent No. 5874243
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Sathe, Ganesh
TITLE OF INVENTION: NOVEL OLRCC15
NUMBER OF SEQUENCES: 2
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US-08-827-291A-1
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                RECEPTOR
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Best Local
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OPERATING SYSTEM: DOS
SOETWARE: FASTSEØ FOR WINDOWS VERSIOI
SOETWARE: FASTSEØ FOR WINDOWS VERSIOI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
APPLICATION NUMBER: DESCRIPTION OPERATOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/NDOCKET NUMBER: GP50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-770-5015
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: SmithKlin
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STREET: 709 Swedeland
CITY: King of Prussia
STATE: PA
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454; Conservative
GACTGCCTTTTCCTGGATCCTGGGCTCTACAGATGGAATCATTTATGCTGTAGCCACATT
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                       gctcagcatggtcatggctattgcagtcaccaattcctgggtgcacacagctcttatcat 482
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pred. No. 1.3e-47;
0; Mismatches 453;
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US-08-748-506-6

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US-08-748-506-6

; Sequence 6, Application US/08748506

; Patent No. 6159707
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                                                                                       TELEFAX: 312-616-5700
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1087
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MOLECULE TYPE:
                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 312-616-5600
                                                                                                                                                        ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ronnett et al. TITLE OF INVENTION: NOVEL
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                          STRANDEDNESS: double
                                         TYPE: nucleic acid
                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                     APPLICATION NUMBER: US 6 FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 08-NO
               TOPOLOGY:
                                                                                                                      TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Leydig, Voit & Mayer, Ltd STREET: Two Prudential Plaza, Suite
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CTATCATCTACAGTCTAAGGAACAAGGAAGTCAAGGCAGCACTGAGAA
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Pred. No. 5e-46;
0; Mismatches 4
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US-08-467-948A-1

Sequence 1, Application US/08467948A Patent No. 5998164
GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

CAO, LIANG NI, JIAN GENTZ, REINER

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LOCATION:
US-08-467-948A-1
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Best Local Similarity
Matches 411; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Polynucleotides Encoding Human TITLE OF INVENTION: Coupled Receptor GPR2 NUMBER OF SEQUENCES: 30
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER,
STREET: 1100 NEW YORK AVE.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PATENTIN REI
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORWATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/467,948A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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STRANDEDNESS: both
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                           acatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctatgtg 363
                                                                CTCCTGCATCCAGCCAAGCCCATCTCCTTTGCTGGTTGCATGACACTAGACTTTCTCTTT
                                                                            atgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttgttc 303
                                                                                                                           CACCTGGCCGTCGTCAACATCGCCTATGCCTGCAACACAGTGCCCCAGATGCTGGTGAAC
                                                                                                                                                                                        ATCCTGGGGCTCATCTCACTGGACTCCAGACTCCACACCCCCATGTACTTCTTCCTCTCA 316
 TTGAGTTTTGCACATACTGAATGCCTCCTGTTGGTGCTGATGTCCTACGATCGGTACGTG
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SUTTON III, GRANGER
ROSEN, CRAIG A.
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 1, Application Patent No. 6090575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
APPLICATION NUMBER: 907-VIS
ETLING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,68
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NUMBER OF SEQUENCES: 30
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MEDIUM TYPE: FLOPPY DISK
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REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
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                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
                                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                           APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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1100 NEW YORK AVE.,
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                                                                                                                                                                                                                                                                                                   USA
                                                                                               OMBER: PCT/US95/04079
30-MAR-1995
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                                           1488.1140002/EKS/KLM
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NW, SUITE 600
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; LOCATION:
US-08-467-947A-1
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SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                   agctatacatttgaaagagacaaggt 809
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CGCCATCCTGAGGAGCAGCAGAAGGT
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                                                                       ATCCTGAGGATCCAGTCTGGGGAGGGCCGCAGAAAGGCCTTCTCCACCTGCTCCCAC
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Pred. No. 5.9e-45;
0; Mismatches 395
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US-08-748-506-9
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 66
FILING DATE: 09-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ZIP: 60601-6780
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TATCTTGTCGTGGGGGCAACAGGTTTTTTCCTTTTGGCTGCGTTATCCCTGGACCGCTTT
                        ttcacatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctat 360
                                                                         accatgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttg
                                                                                                                AGCACCTTCTCTTTTGTGGAGTGTTGTTTTATAACTACTGCTATCCCCCAGCTCCTCACC
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Two Prudential Plaza, Suite
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47.8%;
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Pred. No. 3.3e-37;
0; Mismatches 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
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                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,
FILING DATE: Herewith
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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FILING DATE: ATTORNEY/AGENT INFORMATION
                                                    PRIOR APPLICATION DATA:
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                                     APPLICATION NUMBER:
                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
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Hillman, Jennifer L.
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Best Local Similarity
Matches 356; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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CLONE: 364702
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                                                                                                                                                                      cccattgctggctttgtcctgtagccctgtaagaatcaatgaggtgatggtgtatgttgc 596
                                                                                                                                             TCAACTCTCCCATCTTGCATGTTGTGACACCTTCACCATTAACATAATCATGTATTTCCC
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atctcatctcacagtggt 734
                             TTCCTCCATTCTGAGGGTTTCATCATCAGGTGGGAAGTATAAA-CCTTCTCCACCTGTGG
                                                                                    TGCTGCCATATTTGGTTTTCTTCCCATCTCAGGGACCTTTTCTCTTACTGTAAAAATTCT 1451
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                                            tgttgctattctccgtatccgcacagtagaaggcaagaggaaggccttctcaacatgctc 716
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pred. No. 9.6e-20;
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; ORGANISM: HOMO
US-09-439-313-526
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US-09-439-313-526
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Matches
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LENGTH: 963
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SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 1999-11-12
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ccaatgtggtatatggtcttactgccattctgctggtcatgggcgtggacgtaatgttca
                    tcaatgaggtgatggtgtatgttgctgatattaccctggccataggggactttattctta
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Dillon, Davin
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Retter, Mark
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Pred. No. 2e-17;
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                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                       TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FEITATO, Gregory D.
REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700
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                152 ccttgcatacgcccatgtatgttttccttctgacactggctgttgtggacatcatctgca 211
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                                                                                                           Local Similarity
les 305; Conserv
                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CARELLA, BYRNE, I ADDRESSEE: STUART & OLSTEIN
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GCCTGCACGCTCCGATGTACCTCTTTCTCTGCATGCTTGCAGCCATTGACCTGGCCTTAT
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                                                                                                                        Score 83;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09053303 Patent No. 5948890
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Soppet
                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1031
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/465,980
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen, Craig A. APPLICANT: Ruben, Steven M.
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STUART & OLSTEIN
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REGISTRATION NUMBER: 36,13*
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TWEITEPHONE: 201-994-1700
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SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pair
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Pred. No. 2.5e-16;
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PCT-US95-07093-1
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US OF FILING DATE: 06-JUN-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70 NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen, (APPLICANT: Ruben, CAPPLICANT: RUBEN, CAPPLICANTION:
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hes 305;
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STRANDEDNESS: single
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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atgcaggctgcatgtcccagctcttcttgttcacatggtctctgggagctgagatggttc 331
                                                                                                                                                caacaagcatcataccgaagatgctggggaccatgctaacatcagaaaataccatttcat 271
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                                                                                                                            CCACATCCACCATGCCTAAGATCCTTGCCCCTTTTCTGGTTTGATTCCCGAGAGATTAGCA
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Li, Yi
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RESULT 15
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                                 TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
13200 hase pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                    TELEPHONE: (202) 887-1500
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                            APPLICATION NUMBER: US/08/599,252 FILING DATE: 09-FEB-1996
STRANDEDNESS:
                                                                                      TELEFAX:
                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                  REGISTRATION NUMBER:
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            nucleic acid
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                             1320 base pairs
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FEDER, JOHN N.
GNIRKE, ANDREAS
KIMMEL, BRUCE E.
                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                              2000 Pennsylvania Ave. N.W.,
                                                                                         (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THOMAS, WINSTON J. WOLFF, ROGER K.
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594	521	728	732	660	632	545	752	667	635	634	542	632	752	743	542	634	686	814	680	627	794	605	630	629	805	612	1501
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AZ599283	AZ407823	вн279965	BG068751	AZ380178	AZ648626	AQ389818	вн362510	вн293359	AQ527378	A2507680	AQ632709	A2765752	BH065531	вн322680	AZ252110	BB635510	AZ086625	A2699230	AZ709687	AQ240757	AZ913406	AZ642411	AQ503914	AZ019257	вн272774	AZ396764	AK016338
283	ω							вн293359 Сн230-92С		1M0349L2	RPCI-11-	1M0562E1	RPCI-2	CH230-	RPCI-23-	3B635510	RPCI-23-	RPCI-2	RPCI-24-	CIT-HSP-	RPCI-2	1M0505L2	RPCI-11-	RPCI-2	_	\vdash	AK016338 Mus muscu

ALIGNMENTS

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM RESULT 1
AQ428256
LOCUS
DEFINITION JOURNAL COMMENT REFERENCE AUTHORS FEATURES TITLE source 9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends. Unpublished (1997)
Other GSSs: CITBI-51-2578F11.TR
COntact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research AQ428256 AQ428256.1 1 (bases 1 to 470)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready map Building Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. DNA sequence. AQ428256 470 CITBI-E1-2578F11.TF CITBI-E1 /organism="Homo sapiens"
/db_xref="taxon: 9606"
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Homo sapiens, Similar to olfactory receptor,
member 4, clone IMAGE:4424116, mRNA.
BC016940
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 27 Row: 1 Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                Submitted (05-NOV-2001) National Institutes of Health, Mammalian Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2021)
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                                                                                                          cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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                 CGCCATCCTGAGGAGCAGCAGAAGGTCCTTTTTCTATTTTACAGTTCTTTCAACCCGATG
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438 AATCAGACAATGGTCACAGAGTTCCTCCTACTGGGATTTCTCCTGGGCCCAAGGATTCAG
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   agotatacatttgaaagagacaaggtggtagotgcactctatactcttgtgactcccaca
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4424116"
/tissue_type="Kidney, hypernephroma"
/clone_lib="NHH_MGC_89"
/lab_host="pH10B"
/lab_host="pH10B"
/note="PVector: pCMV-SPORT6"
) a 546 c 427 g 578 t
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Pred. No. 1.2e-40;
0; Mismatches 434;
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Insert Length: 10000 Std Error: (
Plate: 0405 row: K column: 03
Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 580)
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AZ593814
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Fax: 801 585 7177
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University of Utah
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            10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                               (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0405K03"
                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
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Query Match Best Local Similarity

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3.6; DB 1e-37;

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                                                                                                                  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new (Genome Res. 10 (10), 1617-1630 (2000)
Shibata, K. Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
                                                                                                                                                                                                                                                       Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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/clone_lib="RIKEN full-length enriched
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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/protein_id="GI:12855358"
/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL
                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                        /clone="4932441H21"
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VYTMHFPPCMSQBIRHLLCEVPPLLKLACADTSQYELMVYVTQVTFLLLPLSAIITSY
SLILFTVLHMPSNEGRKKALVTCSSHLTVVGMFYGGATFMYVLPSSFHSPKQDNIISV
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Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933433E02:similar to Tl OLFACTORY RECEPTOR, full
                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                                          Hayashizaki,Y
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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catgctaacatcagaaaataccatttcatatgcaggctgcatgtcccagctcttcttgtt 302
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448; Conser
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18.8%;

Score 173.8; DB 1 Pred. No. 8.1e-34; Mismatches

DB 11;

Length 1394;

0;

Gaps

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462

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Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-kı, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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SAMTLGGAEDLLLAFMAYDRŸVAIĞHPENYMIFMSPKACREMVAISWILASLSALĞHT
VYTMHEPFCMSQEIRHLLCEVPPLLKLACADTSQYELMYVVTCVIFLLLPLSAIITSY
SLILFTVLHMPSNEGRKKALVTCSSHLTVVGMFYGGATFMYVLPSSFHSPKQDNIISV
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337 c 304 g 398 t
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/translation="MERMNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL
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                                                                                                                                                                                                                                                                                                                                     /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                similar to T1 OLFACTORY RECEPTOR"
                                                                                                                                                                                                                                                                           putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
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/clone="4933433E02"
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                        The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200
                                                                                         Mouse BAC End Sequences from Library Unpublished (1999) Other_GSSs: RPCI-23-16619.TV
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                                                              Contact: Shaying Zhao
Department of Eukaryotic Genomics
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TATCCTTGTGCCCAGCATCACCATTTTTATCTCTTATGGGTTCATTCTCTCCAGCATTTT
                                                         ggccataggggactttattcttacctgcatctcctatggttttatcattgttgctattct
                                                                                                                         GCTCTCCTGCACCAGCACCTATGTCAATGAACTGGAAGTTTTCATTGTCGTGGGCATCAA
                                                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 166 row: I column: 9
seq primer: SP6
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//lab_host="DH10B"
//lab_host="Corran: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Site_2: Corrange of the pBACe3.6; Vector at the gelected DNA was cloned into the pBACe3.6; Vector at the georg sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
//note="Organ: pBACe3.6; Site_1: pBACe3.6; Site_1: page of the pBACe3.6; Site_1: page of the pBACe3.6; Site_2: page of the pBACe3.6; Site_1: page of the pBACe3.6; Site_2: page of the pBACe3.6; Site_1: 
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/clone="RPCI-23-16619"
/clone_lib="RPCI-23"
/sex="Female"
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                                                                                            164 ccatgtatgttttccttctgacactggctgttgtggacatcatctgcacaaccaagcatca
                    | 224 taccgaagatgctggggaccatgctaacatcagaaaataccatttcatatgcaggctgca 283
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61
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                                                                      CAATGTACTTTTTCCTTTTTAACTTGTCATTTGTTGACCTCTGGTACTCTTCAGTGTTCA 60
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CACCCAAAATGCTGATGA-GTTTATATCAGAGAAGAACATTATTACCTACAAAGGATGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Szhao@tigr.org
Email: Szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 51 row: L column: 13
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Rat BAC End Sequences from Library CHORI-230 I
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CH230-51L13.TV CHORI-230 Segment 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: BAC ends
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Department of Eukaryotic Genomics
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Other_GSSs: CH230-51L13.TJ
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                             /cell_type="Brain"
/note="Vector: pTaRBAC2.1; Site_1:
/note="Vector: pTaRBAC2.1; Site_1:
CHORI-230 Rat (BN/SSNHSd/MCW) BAC 1
Pieter de Jong"
a 152 c 108 g 214 t
                                                                                                                                                                                                                                                                                                                                                                                                   /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-51L13"
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                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
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57.0%;
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I (bases 1 to 762)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,C., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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RST12467
BG193339
                                                                                                                                                                                                                                                               Athersys, Inc.
3201 Carnegie Ave,
Tel: 216 431 9900
                                                                                                                                                                                        Email: scain@athersys.com
High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Athersys RAGE Library
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily
                                                                                              /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone_lib-"Athersys RAGE Library"
/cell_line-"HT1080"
                                                                                                                                                                                                                                                                                    Cleveland,
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Best Local Sim
Matches 394;
                  ACCESSION
VERSION
KEYWORDS
SOURCE
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BH069789/c
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                                          BH069789
BH069789.1 GI:14889386
                                                               698 bp RPCI-24-331A10.TVB RPCI-24 Mus RPCI-24-331A10, DNA sequence.
Eukaryota;
          Mus musculus
                     house mouse.
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milarity 54.0%;
Conservative
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156 g
  Chordata;
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Pred. No. 3.5e-33;
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 Craniata;
                                                                             musculus
                                                                                         DNA
    Vertebrata;
                                                                              genomic
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    Euteleostomi;
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AUTHORS
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TGTGGGGACAGCTACATTCAAGAGGTGGTGATAATTGTTTTTGCCATTTTTGTCATGCCT
                          tgtagccctgtaagaatcaatgaggtgatggtgttgtgtgctgatattaccctggccata
                                                                                TGTGGAAACAATGAGATCAATTTCATATTCTGTGACCTCCCCCCATTGTTAAAACTCGTA
                                                                                                    tgtgggccaaacaccattgaccacttcttctgtgagatacccccattgctggctttgtcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the mouse BAC library RPCI-24. For E library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). B page: http://www.tigr.org/tib/bac_ends/mouse/bac_end_intro.h plate: 331 row: A column: 10 seg_primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Mouse BAC End Sequences from Library RPCI-24
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Other_GSSs: RPCI-24-331A10.TJB
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-331A10"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA.
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/note="Vector: pTARBACI; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBACI; Site_1: BamH1; The
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
Library was cloned in the pTARBACI cloning vector at the
Library was cloned in the pTARBACI cloning vector at the
RamH1 sites using MboI partially digested male C57BL/6J
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Pred. No. 6.2e-33;
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                                                                                                                                                                                                                                                                                                                         Seq proclass:
                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@rmed.edu.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 33 row: G column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC Clones are derived from the mouse BAC library RPCI-23.
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Other_GSSs: RPCI-23-33G18.TJ
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RPCI-23-33G18.TV
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     206
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     Q
                 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                   /lab_
                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-33G18"
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                                                                                                                                                                       /sex="Female"
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Sciurognathi; Muridae;
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                                 Unpublished (1999)
Other_GSSs: CH230-46N15.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                              Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                            CH230-46N15.TV CHORI-230 Segment 1 CH230-46N15, DNA sequence.
                                                                                                                                  Rat BAC End
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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                                                                                                             Sequences from Library CHORI-230 (1999)
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                 Center Dr., Rockville,
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Pred. No. 1.4e-31;
0; Mismatches 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact pleter de Jong (pdejong@mail.cho.org). clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                       tgtgtgtagccttgctcagcatggtcatggctattgcagtcaccaattcctgggtgcaca 469
                                                                                                                                                                                                                                                                                                                                                                                    ATGATAGGTTTGTGGCTATCTGTCATCCACTGAGGTACACTGTCATTATGAATCCCAAAT 372
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                                                                                                                                                                                                                                                                                                                     TCTGTGGTGTGATGCTTTTGTTGTTCTTCTTGATAAGCATTCTAGATGCTTTGCTCCACA
                                                                                                                                                                                                   agatacccccattgctggctttgtcctgtagccctgtaagaatcaatgaggtgatggtgt 589
                                                                                                                                                                                                                                                   CTTTGATGGCACTGCGCCTGTCATTCTGCACAAAGGTGGAAATTCCTCACTTTTTTTGTG
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Class: BAC ends.
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                                                                       ttatcattgttgctattctccgtatccgcacagtagaaggcaagaggaaggccttctcaa
                                                                                                                  ATTTGGTGACAAGTCTGTTGGGTGTTCTTCCACTGTCTGGTATAATTTATTCTTATACTA
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                                                  GAATTATTTCCTCTGTTTTGAAAATTCCATCAGCTGCAGGAAAATATAAAGTTTTCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by Pieter de Jong"
172 c 158 g 313 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="BN/SSNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-46N15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CHORI-230 Segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-ANG-2001) Asao Fujiyama, The Institute of Physical Submitted (02-ANG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (95), Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chimpbasegescriken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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AG167722.1 GI:16697400
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43
Male BAC Library clone:RP43-035001.TJ.
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tctatagcaacaccttgcatacgcccatgtatgttttccttctgacactggctgttgtgg
                                                                 TGTTTTTGTCCTTCTACATCTTCACCGTTATGGGGAACCTGCTCATCTTGCTGGCTATTG 142
                                                                                                        tttttctcattgtctatcttgtggcttttctcggcaacatgctcatcatcattgccaaaa 139
                                                                                                                                                      CTTTANTTATCCTGCTGGGCACCCCTCACATGGAGGGTCTGGAGACTATGCTCTTGGTCC 82
                                                                                                                                                                                     ctgagttoattattctgggcctcaccaaaaagcctgaactccagggaattatcttcctct 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY
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R.Site 2 : ECORI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-035001.TJ"
                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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pred. No. 4.1e-30;
0; Mismatches 311;
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                                                                                                                                                                                              Contact: Robert B. University of Utah University of Utah
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642 bp DNA linear GSS 27-APR-200200241J24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0241J24 R, DNA sequence.
                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0241 row: J column: 2
                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                     plasmid inserts
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Mammalia; Eutheria;
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GSS.
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                                                                                         Seq primer: CACACAGGAAACAGCTATGACC
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                                                   quality sequence stop:
Location/Qualifiers
                                                                                                                                                                         USA
                                                                              plasmid ends
                                                                                                                                                                                     Biomedical
/organism="Mus musculus
/strain="C57BL/6J"
/db_xref="taxon:10090"
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Rodentia;
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column: 24
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130
                                                                                                                                                                                                                                                                                                                      was hydrodynamically sheared by repeated passage throug 0.005 inch orifice at constant velocity. The sheared DN was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 10.5 kb range using preparative agarces.
                                                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

166 c 129 g 217 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UUGC2M0241J24"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. coli strain XL10-Gold, T1-resistant
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17.0%; 52.9%;

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224 taccgaagatgctggggaccatgctaacatcagaaaataccatttcatatgcaggctgca atactcttgtgactcccacattaaacccgatggtgtaca tgcacacagctcttatcatgaggttgactttctgtgggccaaacaccattgaccacttct tggcctatgaccgctatgtggccatttgtttcccttcttcattacagtactattatgaacc TCCCCCAGATGATGGTGCATCTTCTGTCAGAGAAAAATCATTTCCTATGGAGGCTGTG cctatatccgccctgcttccagctatacatttgaaagagacaaggtggtagctgcactct TTTCCACCTGTGCCTCCCACCTGCTCATTGTTATTCTCTATTATGGCAGTGCTATCTTCA totcaacatgctcatctcatctcacagtggtgaccctttactattctcctgtaatctaca ACCTTTACATCATCTCCACCATCCTGAGGATCCGTTCCTCTGAGGGGAGGCACAAAGCCT atggttttatcattgttgctattctccgtatccgcacagtagaaggcaagaggaaggcct CTTTGCTGTCCATTGGGATCCTCATAGGCTGGACTCCTTTCCTGTGCGTCATCCTTTCCT AGGCTCTGTGCAGCTGGTTAGCAGCTTCATGCTGGACAGGTGGGTTTCTCAACTCAGTGT accatatgtgtgtagccttgctcagcatggtcatggctattgcagtcaccaattcctggg TGGCATATGATCGATATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACA TGACCCAGCTCTTTGCATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAA tggtgtatgttgctgatattaccctggccataggggactttattcttacctgcatctcct TCTGTGACATACCTCCCTTGCTCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGG TGCACACGGTTTTGACCTTCCACCTGCCCTTTTGTGGTAACAATCAGATCAATTATTTCT tgtcccagctcttcttgttcacatggtctctgggagctgagatggttctctttcaccacca Conservative 0; Score 157.4; DB Pred. No. 1e-29; O; Mismatches 3 301; 862 Indels 0; Gaps 823 583 523 180 403 600 540 763 480 703 420 643 360 240 463 343 60 300 283 0

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465 TCTAATAGCAGATGTCTTCTATGGAGGCATCAATTTTGTGCTTACCTTACCTATCCTATGG
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nes 275; Conserv
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RPCI-23-333010.TV RPCI-23
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
1 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
[plateredejong.med.buffalo.edu). Clones may be purchased from
[plateredejong.med.buffalo.edu]. BAC end page:
[provide of the provide of the provide of the page of the provide of the page of
                                                             gtatgttgctgatattaccctggccataggggactttattcttacctgcatctcctatgg
                                                                                                                                     TGAGATTCCCCCACTCCTTCTGCTCTCCTGTAGCCCCACATACGTAAACAGCATTATGAC
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Unpublished (1999)
Other_GSSs: RPCI-23-333010.TJ
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Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shazhao,S., Nierman,W., Feldblyum,T., Malek,J., Shazhao,S., Tsegaye,G., Geer,K.,
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Department of Eukaryotic Genomics
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/strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="RRCI-23-333010"
/clone_lib="RPCI-23"
/sx="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or EcoRI; Site with a combination of EcoRI and EcoRI Methylase. Size with a combination of EcoRI onto the pBACe3.6 vector at the selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). The DH10B electrocompetent cells (BRL Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 156.6; DB 12;
Pred. No. 1.6e-29;
0; Mismatches 180;
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                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 CGCCATTGGCAGGCTCTTGCCCTCTTTCTCACATTA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACCTGCTCATCCCACCTCATCGTGGTCTCTGTGTACTACTCATCTGTGTTCTGTGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aacatgeteateteateteacagtggtgaecetttaetatteteetgtaatetaeaeeta 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tottgtgactcccacattaaacccgatggtgtacagcttccagaatagggagatgcaggc 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCAGCCCTGCATCCAGCTATAGCCCCAGAAAGAAGCAAAGTTACCTCTGTGTTGTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aqgaattaggaaggtgtttgcatttctgaaacacta 923
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                                     4 aatcacagcgttgtaactgagttcattattctggggcctcaccaaaaagcctgaactccag
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, C., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M., Creation of genome-wide protein expression libraries using random activation of gene expression activation of gene expression
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BG197640
RST17016 Athersys RAGE Library I
BG197640
BG197640.1 GI:13719455
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Tel: 216 431 9900
Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: scain@athersys.com
High quality sequence stop:
    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21227151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1_to 796)
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                   a
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/cell_line="HT108
                                                                                                                                                       16.8%;
                                                                                                                              score 155.6; DB 1
Pred. No. 3.2e-29;
0; Mismatches 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
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                                                                                                                                                                                            DB 10;
                                                                                                                                        360;
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                                                544 ctggctttgtcctgtagccctgtaagaatcaatgaggtgatggtgtatgttgctgatatt 603
                                                                                                                                                                                                                                                                                                                                                                     304 acatggtctctgggagctgagatggttctcttcaccaccatggcctatgaccgctatgtg 363
                                                                                                                                                                                                                                                                                                                                                                                                                          565 TTGAAGTTGGCCTGTGGAAATAATGTACCAGCTGTGGCCCTGNGCGTGGGCTTGGTATGT
                                                                                                                                                                                                             505 CAACTGACTTTCTGTGGATTCCAAGAGATCCAGCATTTTTTATGTCATGTGCCACCTCTG
                                                                                                                                                                                                                          484 aggttgactttctgtggggccaaacaccattgaccacttcttctgtgagatacccccattg 543
                                                                                                                                                                                                                                                                                 424 ctcagcatggtcatggctattgcagtcaccaattcctgggtgcacacagctcttatcatg 483
                                                                                                                                                                                                                                                                                                                     385
                                                                                                                                                                                                                                                                                                                                 364 gccatttgtttccctcttcattacagtactattatgaaccaccatatgtgtgtagccttg 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145
745 CACCTTAATTGGGTCATTGTGCACTAT 771
                       721 catctcacagtggtgaccctttactat 747
                                                                                                                                                                                                                                                               445 GIGGGCTGCTCCTGGGCTGGTGGCTCGGCCATGGGGATGGTGGTGACCTCGGCCATTTTC 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ggaattatcttcctcttttttctcattgtctatcttgtggctttttctcgggcaacatgctc
                                                                                                                                                                                                                                                                                                                   ATCATGGCCACCGTCTGGAGCGAGCGCAGCCTCCACACGCCCATGTACCTCTTCCTGTGC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGATGCTCTTCCTGCTGTTCCTGCTGATGTACCTGTTCACGCTGCTGGGCAACCTGTTC 144
                                                                                                                                                         624
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learch completed: June 21, 2002, 11:53:48
Job time: 9626 sec

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307. 307.

.0e-09 0e-09 0e-09

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Database sequences: 383533
Database length: 122816752
Search time (sec): 48.290000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query length: 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
Query: US-09-975-308-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=USO9975308_@CGN1_1.111 -NCPU=6 -ICPU=3 -LONGLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _6/ptodata/1/ina/6A_0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ptodata/1/ina/5B_COMB.seq:US-08-827-291A-1 + 598.00 1172.75 1
/ptodata/1/ina/6B_COMB.seq:US-09-085-371-5 + 596.50 1173.75 1
/ptodata/1/ina/5B_COMB.seq:US-09-085-371-5 + 596.50 1173.75 1
/ptodata/1/ina/5B_COMB.seq:US-08-467-947A-1 + 577.50 1128.47 3
/ptodata/1/ina/6A_COMB.seq:US-08-467-947A-1 + 577.50 1128.47 3
/ptodata/1/ina/6A_COMB.seq:US-08-748-506-9 + 524.00 1027.31 1
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/ptodata/1/ina/6B_COMB.seq:US-09-499-313-526 + 374.00 726.62
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7 3.6e-55
1.6e-49
3.1e-35
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; MOLECULE TYPE:
US-08-748-506-6
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US-09-975-308-9
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/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-228-932-5 +
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-468-939-5 +
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-406-855A-5 /
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-722-190-5 +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
63 LeuAlaValValAspIleIleCysThrThrSerIleIleProLysMetLe 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08748506 Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION DATA:
APPLICATION USATA:
APPLICATION 0ATA:
APPLICATION UMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELEPHONE: 312-616-5600
TELEPHONE: 312-616-5700
TELEPHONE: 312-616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
164 NTTGTACCAGTCCATCTCTACACACCCCCATGTACTTCTTCTGGCCAAC
                                                                                   114 TCTCATGTTCTTAGTATCACTAACAGGAAATGCTCTCATAGCCCTTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: THE Chicago
                                     46 ysileTyrSerAsnThrLeuHisThrProMetTyrValPheLeuLeuThr 62
                                                                                                                        29 uIleValTyrLeuValAlaPheLeuGlyAsnMetLeuIleIleIleAlaL 46
                                                                                                                                                                  64 AAGTTCTCTGAGGTCCCTGGAGAATGCTTCCTCCTGTTCACCCTCATCCT 113
                                                                                                                                                                                                16 LysLysProGluLeuGlnGlyIleIlePheLeuPhePhe.....Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Two Prudential Plaza, Suite 4900
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2.887
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seq_documentation_block:
; Sequence 5, Application
; Patent No. 6159707
                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-748-506-5
                                                                                                                                                            Sequence 5, Application US/08748506 Patent No. 6159707
                                                                                                         GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                      290 lnAsnArgGluMetGlnAlaGlyIleArgLysValPheAlaPheLeuLys 306
                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDAGE INC
STREET: INC
STRY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCAACCCGAATGAGTCGTGAGGTATGTGCCCATTTGGCAATTGTTTCAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCCATGGCCTTTGACCGCTGCATGGGCATATGCTCCCCACTCCACTA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrThrMetAlaTyrAspArgTyrValAlaIleCysPheProLeuHisTy 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::|||:::|||:::||||:::
CACAGATGTTTTTCACATTTTTTGGCATAACTGAGTGCTGCCTATTG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uGlyThrMetLeuThrSerGluAsnThrIleSerTyrAlaGlyCysMetS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThralaLeuIleMetArgLeuThrPheCysGlyProAsnThrIleAspHi 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGAATGGGATGCATAGTAGGTCTGGGACAGACCAATTTN......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPhePheCysGluIleProProLeuLeuAlaLeuSerCysSerProVala 190
|||||||||||::::::|||||||||||||||||:::|||:::
CTTCTTCTGTGACCTTCCACCTCTCCTGGCACTTGCCTGTGGTGATACAT 595
                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspPheIleLeuThrCysIleSerTyrGlyPheIleIleValAlaIleLe 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....LeuSerMetValMetAlaIleAlaValThrAsnSerTrpValHis 156
                                                                                                                                                                                                                                                                                                                                                                                                                                            IleArgProAlaSerSerTyrThrPheGluArgAspLysValValAlaAl 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACACCTACTTGTAGTCACACTCTTTATGCCTCTGTGTCCTTTACCTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgIleAsnGluValMetValTyrValAlaAspIleThrLeuAlaIleGly 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....ATTTNCTCCTTGAACTTCTGTGGACCTTGTGAGATAGACCA 545
                                                                                                                                                                                                                                                                       TIGAGGCCCAAGICTAGCCACTCACCAGGAAIGGACAAACICTIGGCCCT 845
                                                                                                                                                                                                                                                                                                                                            CTTCTACACAGCAGTGACATCCATGCTGAACCCTATCATCTACAGTCTAA 895
                                                                                                                                                                                                                                                                                                                                                                 aLeuTyrThrLeuValThrProThrLeuAsnProMetValTyrSerPheG 290
                                    E: Leydig, Voit & Mayer, Two Prudential Plaza, Su
                                          er, Ltd.
Suite 4
                                             4900
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TOPOLOGY: 1i;

MOLECULE TYPE:
US-08-748-506-5
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US-09-975-308-9 x US-08-748-506-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION BATA:
APPLICATION NUMBER: US 60/033,751
PRIOR APPLICATION DATA:
APPLICATION 1435
CLASSIFICATION 345
CLASSIFICATION 435
CLASSIFICATION 435
CLASSIFICATION 1436
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
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Percent Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
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                                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                65 lvalAspIleIleCysThrThrSerIleIleProLysMetLeuGlyThrM 82
                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 AATAGTTTGACTGTCAAACACTTT......GCATTTGCCAAGTTCTC 71
                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                               oGluLeuGlnGlyIleIlePheLeuPhePhe......LeuIleValT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnHisSerValValThrGluPheIleIleLeuGlyLeuThrLysLysPr
                                                                                                                                                                                                                                                                                                      tAlaTyrAspArgTyrValAlaIleCysPheProLeuHisTyrSerThrI 132
                                                                                                   PhoLeuPheThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMe 115
                                                                                                                                                                                               etLeuThrSerGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeu 98
leMetAsnHisHisMetCysValAlaLeuLeuSerMetValMetAlaIle 148
                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    622.00
2.777
72.727
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Percent Identity: 41.883
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6:
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seq_documentation_block:
   Sequence 7, Application US/08748506
   Patent No. 6159707
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MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      622
                                                                                FILING DATE: 08-NOV-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672
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                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 TyrSerProValIleTyrThrTyrIleArgProAlaSerSerTyrThrPh 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 rgLysAlaPheSerThrCysSerSerHisLeuThrValValThrLeuTyr 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 AlaAspIleThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 ArgLysValPheAlaPheLeuLys 306
ATTORNEY/AGENT INFORMATION:
                    APPLICATION NUMBER: US 60 FILING DATE: 09-NOV-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                      STREET: Two P
                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGAATGGACAAATTCTTGGCCCTCTTCTACACAGTAGTGACATCCATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eGluArgAspLysValValAlaAlaLeuTyrThrLeuValThrProThrL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGGCTCAGCATGTATTACCTATTTGAGGCCCAAGTCTAGCCACTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGCAGTCCTCTGCATATCTAGCCCCATTTTTGCTGATCATTTATTCTTA
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                                                                                           US/08/748,506

08-NOV-1996

ON: 435
                                                              US 60/033,751
                                                                                                                                                                                              Version
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; MOLECULE TYPE: US-08-748-506-7
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                        414
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LENGTH: 966 base pairs
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                                                                                194 alMetValTyrValAlaAspIleThrLeuAlaIleGlyAspPheIleLeu
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211 ThrCysIleSerTyrGlyPheIleIleValAlaIleLeuArgIleArgTh
                                                                                                                                                                                                                                                                                                                                           144 etValMetAlaIleAlaValThrAsnSerTrpValHisThrAlaLeuIle 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LysLysProGluLeuGlnGlyIleIlePheLeuPhePhe.....Le
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                                                                                                                                                                                                                  TTCTCCTTGAACTTCTGTGGACCCTGTGAGATAGACCACTTCTTCTGTGA
                                                                                                                                                                                                                                      MetArgLeuThrPheCysGlyProAsnThrIleAspHisPhePheCysGl 177
                                                                                                                                                                                                                                                                                                                                                                                     TGCAACCCGAATGAGTCGTGGGGTATGTGCCTATTTGGCAATTGTCTCAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrThrMetAlaTyrAspArgTyrValAlaIleCysPheProLeuHisTy 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuAlaValAspIleIleCysThrThrSerIleIleProLysMetLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ulleProProLeuLeuAlaLeuSerCysSerProValArgIleAsnGluV
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                                          CTGCCATCTTTGTGGCAGCAGTGCTCTGCATATTTAGTCCATTTTTACTG
                                                                                                                                                                                                                                                                                                   GGGTGATGGGATGCATAGTA.....GGTCTGGGACAGACCAATTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                              rSerThrIleMetAsnHisHisMetCys.....ValAlaLeuLeuSerM 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGCCATGGCCTTTGACCGCTATATGGCTATATGTTCCCCCACTCCACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTCTCTCCTGGAGATTGGCTATACTTGCTCTGTCATACCCAAGATGCT 263
                                                                                                                             CCTTCCACCTCTCCTGGCACTTGCCTGTGGTGATACATCCCAAAATGAGG
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Ratio:
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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-748-506-8
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                                                                                                                                       ; MOLECULE TYPE: US-08-748-506-8
alignment_block:
                                                                                      alignment_scores:
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                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEPAX: 312-616-5700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Pr
CITY: Chicago
STATE: IL
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                        Quality:
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                                                                                                                                                           DNA (genomic)
                                      614.50
2.845
72.973
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                                       Percent Identity:
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                                                                            Length:
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43.581
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Align seg 1/1 to: US-08-748-506-8 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etValMetAlaIleAlaValThrAsnSerTrpValHisThrAlaLeuIle 160
                                                                                                                                                                                                                                                                                                                                                                                        ulleProProLeuLeuAlaLeuSerCysSerProValArglleAsnGluV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetArgLeuThrPheCysGlyProAsnThrIleAspHisPhePheCysGl 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTGATGGGATGCATAGTA.....GGTCTGGGACAGACCAATTTTATT 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rSerThrIleMetAsnHisHisMetCys.....ValAlaLeuLeuSerM 144
                                                                                                                                                                                                  ThrCysIleSerTyrGlyPheIleIleValAlaIleLeuArgIleArgTh
                                                                                                                                                                                                                                                                                                                  CTGCCATCTTTGTGGTAGTTGTCCTCTGCATATCTAGCCCTTTTTTGCTG
                                                                                                                                                                                                                                                                                                                                             alMetValTyrValAlaAspIleThrLeuAlaIleGlyAspPheIleLeu
                                                                                                                                                                                                                                                                                                                                                                         TCTTCCACCTCTCCTGGCACTTGCCTGTGGTGATACATCCCAAATTGAGG
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                                                                                   alValThrLeuTyrTyrSerProValIleTyrThrTyrIleArgProAla 260
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| AGTGACATCCATGTTGAACCCTATCATCTATAGTTTAAGGAACAAGGATG
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                                                                                                           SerSerTyrThrPheGluArgAspLysValValAlaAlaLeuTyrThrLe 277
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TCAAGGCAGCAGCTGAGAAGAATTCTGGCCCTGAAAAAA 945

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alignment_block:
US-09-975-308-9 x US-08-827-291A-1
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; MOLECULE TYPE:
US-08-827-291A-1
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                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-827-291A-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GP50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610.270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Macina, Roberto
APPLICANT: Sathe, Ganesh
TITLE OF INVENTION: NOVEL OLCC15 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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52 LeuHisThrProMetTyrValPheLeuLeuThrLeuAlaValValAsp..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
FILING DATE: 28-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19406
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2.682
73.841
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-085-371-5
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                                                                                                                                                                                                                                                                                                                                                         1052 GGAGCAGGTTTGTTCATGTACATACAGCCCACATCTGATCGCTCCCCAAC 1101
                                                                                                  300 Lysval 301
                                                                                                                                                                                283 snProMetValTyrSerPheGlnAsnArgGluMetGlnAlaGlyIleArg 299
                                                                                                                                                                                                                                                                                                   266 uArgAspLysValValAlaAlaLeuTyrThrLeuValThrProThrLeuA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                          902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          852 TCCTCTCATGCAATGACACATCAATATTTGAAAAGGTTATTTTCATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 laLeuSerCysSerProValArgIleAsnGluValMetValTyrValAla 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 ValThrAsnSerTrpValHisThrAlaLeuIleMetArgLeuThrPheCy 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 TTCTATACATCACTGCTTGGCTCTGAATGCTTTCTTTTGGCTGTTATGGC
                                                                                                                                                    ATCCCCTCATCTACAGCCTCCGCAACAAGGAAGTGACCAGAGCATTCATG 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGlyProAsnThrileAspH1sPhePheCysGluIleProProLeuLeuA 183
|||| ::: ||| ||||||||||||:::||| |||||||
TGGGTCTCGGGAAATAGCCCACTTCTTCTGTGAGTTACCTTCCCTACTAA 851
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                                                                                                                                                                                                                                                                                                                                                                                                        SerProValIleTyrThrTyrIleArgProAlaSerSerTyrThrPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yPheIleIleValAlaIleLeuArgIleArgThrValGluGlyLysArgL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTATAGTAATGCTTGTTTTCCCTGTTGCAATCATCATTGCTTCCTATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euThrSerGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeuPhe
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                                                      1207
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seq_documentation_block:

Sequence 5, Application US/09085371 Patent No. 6218358

GENERAL INFORMATION:
APPLICANT: Firestein, Stuart
APPLICANT: Zhao, Haiqing

TITLE OF INVENTION:

Functional Expression of,

and Assay for,

Functional Cellular

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; TYPE: DNA
; ORGANISM: Rat
US-09-085-371-5
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Quality:
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SEQ ID NO 5
LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-085-371-5 from: 1
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US-09-975-308-9 x US-09-085-371-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/085,371
CURRENT FILING DATE: 1998-05-19
PRIOR APPLICATION NUMBER: US 08/891,243
PRIOR FILING DATE: 1997-07-10
PRIOR APPLICATION NUMBER: US 60/045,961
PRIOR APPLICATION NUMBER: US 60/045,961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 roLeuLeuAlaLeuSerCysSerProValArgIleAsnGluValMetVal 196
                                                                                                                                  463
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                                                                                                                                                                                                                                                                                                                                                                                                                              84 hrSerGluAsnThr......IleSerTyrAlaGlyCysMetSer 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrLeuHisThrProMetTyrValPheLeuLeuThrLeuAlaValValAs 67
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                                                                                                                                                                                                                                 erThrIleMetAsnHisHisMetCysValAlaLeuLeuSerMetValMet 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn version 3.0
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2.854
70.608
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1997-05-07
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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-467-948A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application Patent No. 5998164
GENERAL INFORMATION
                                                                                              NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                               TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       663 ATCCTACATGGCCATCACAGGTGCTGTGATGCGCATCCCCTCAGCTGCTG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 TyrvalalaAspIleThrLeuAlaIleGlyAspPheIleLeuThrCysIl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: BULT, CAROL J.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::|||:::
813 AGCTTTTGACACCAACAAGCTGGTCTGTACTCTACGCTGTCATTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 LeuTyrTyrSerProVallleTyrThrTyrIleArgProAlaSerSerTy 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 rThrpheGluArgAspLysValValAlaAlaLeuTyrThrLeuValThrp
                                                                                                                                                                                                                                   FILING DALL: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
APPLICATION NUMBER: PCT/US95/04079
APPLICATION NUMBER: 30-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                               FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVE., NW, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eSerTyrGlyPheIleIleValAlaIleLeuArgIleArgThrValGluG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGTCCTGGCCATTTTTATTCTGCTGGGACCGCTCTCTGTCACTGGGGC 662
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| CGTTGTTCAATCCCATCATCTACTGCTTGCGCAACCAA 900
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STRANDEDNESS:
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nucleic acid
)EDNESS: both
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CAO, LIANG
NI, JIAN
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CDNA

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alignment_block:
US-09-975-308-9 x US-08-467-948A-1
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Quality:
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; LOCATION:
US-08-467-948A-1
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Percent Similarity:
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                                    210 uThrCysIleSerTyrGlyPheIleIleValAlaIleLeuArgIleArgT 227
                                                                                                                          194 ValMetValTyrValAlaAspIleThrLeuAlaIleGlyAspPheIleLe
                                                                                                                                                                                                                                                                                      160 eMetArgLeuThrPheCysGlyProAsnThrIleAspHisPhePheCysG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               487
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  763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 pArgTyrValAlaIleCysPheProLeuHisTyrSerThrIleMetAsnH 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 ThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMetAlaTyrAs 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 oGluLeuGlnGlyIleIlePheLeuPhePheLeuIleValTyrLeuValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AsnHisSerValValThrGluPheIleIleLeuGlyLeuThrLysLysPr
                                                                                                                                                                                                                 luIleProProLeuLeuAlaLeuSerCysSerProValArgIleAsnGlu 193
                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCCTATGCCTGCAACACAGTGCCCCAGATGCTGGTGAACCTCCTGCATC 386
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                                                                                                                                                                                                                                                               CCTAAGACTGCCCTTTTGTGGGCCTCGTGAAATCAACCACTTCTTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGGTACGTGGCCATCTGCCACCCTCTCCGATATTTCATCATCATGACCT 536
GGTGCTGGTCTCCTACTCACACCTCGGGGGGGCATCCTGAGGATCCAGT
                                                                                                                                                                        AAATCCTGTCTGTCCTCAGGCTGGCCTGTGCTGATACCTGGCTCAACCAG
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                                                                                                                                                                                                                                                                                                                                                  ...TCCTGGACATGTGGCTCCCTCCTGGCTATGGTCCATGTGAGCCTCAT
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68.687
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; NAME/KEY:
; LOCATION:
US-08-467-947A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-467-947A-1
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                                                                                                                                                                                                                                     TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/467,947A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: PCT/US95/04079 APPLICATION NUMBER: PCT/US95/04079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-P
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           863
                                                                       FEATURE:
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 hrValGluGlyLysArgLysAlaPheSerThrCysSerSerHisLeuThr
                                                                                                MOLECULE TYPE:
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                                                                                                                    TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                         LENGTH:
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NI, JIAN
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alignment_scores:

Quality:

577.50

Length:

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Align seg 1/1 to: US-08-467-947A-1 from: 1
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260 aSerSerTyrThrPheGluArgAspLysValVal...AlaAlaLeuTyrT
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                                                                                                                                                                              hrValGluGlyLysArgLysAlaPheSerThrCysSerSerHisLeuThr 243
                                                                                                                                                                                                                                                               uThrCysIleSerTyrGlyPheIleIleValAlaIleLeuArgIleArgT
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                                            GTAGTGGGACTCTTTGGSAGCGCCATCGTCATGTACATGGCCCCTAA 912
                                                                                                                                    CTGGGGAGGCCGCAGAAAGGCCTTCTCCACCTGCTCCTCCCACCTCTGC
                                                                                                                                                                                                                                                                                                                  GTGGTCATCTTTGAAGCCTGCATGTTCATCCTGGTGGGACCACTCTGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ...TCCTGGACATGTGGCTCCCTCCTGGCTATGGTCCATGTGAGCCTCAT
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Percent Identity: 42.424
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
US-08-748-506-9
                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-975-308-9 x US-08-748-506-9
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                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-748-506-9
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08748506 Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: RONNett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 1
FILING DATE: 08-NOV-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  131
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                        35 laPheLeuGlyAsnMetLeuIleIleIleAlaLysIleTyrSerAsnThr 51 ::::::
                                                                                    81 GCACCTGAAGATCCTCTTCCTACTGCACTTGCTGGCCTACTTGGCCT 130
                                                                                                                           18 oGluLeuGlnGlyIleIlePheLeuPhePheLeuIleValTyrLeuValA 35
                                                                                                                                                                        31 AATGGGACTTTGGTCCTGGAGTTCATCCTTGAGGGGTACCCTGTGGCCGA 80
                                                                                                                                                                                                               2 AsnHisSerValValThrGluPheIleIleLeuGlyLeuThrLysLysPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/033,751 FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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CCCTCATGGGCAACATGCTCATAATTACCATCACCTGTGTGGACCACCGA 180
                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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Two Prudential Plaza, Suite 4
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312-616-5700
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08-NOV-1996
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2.449
70.164
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LeuHisThrProMetTyrValPheLeuLeuThrLeuAlaValValAspIl

230

TTGTTTTATAACTACTGCTATCCCCCAGCTCCTCACCATCATTCTGTCAG 280

eIleCysThrThrSerIleIleProLysMetLeuGlyThrMetLeuThrS 85 CTGCAGACGCCCATGTACTTCTTCTCAGCACCTTCTCTTTTGTGGAGTG

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seq_documentation_block:
Sequence 2, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-988-876-2
                                                                                                                                                                                                                                                                                                                                                                     881 TCATCTACACCCTGCGCAACAAGCAGGTCCACCAGGCTCTCAGGGATGCT 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      831 CAGAGAGGCTCTTGTGAACATGGTTGTGACACCCCTTCTGAACCCTG
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                                APPLICANT:
                                                      APPLICANT:
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        APPLICANT:
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                                                                                                                                                                                                                                                                 CTGTCCAGGCTTCAA 945
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Bandman, Olga
Hillman, Jennifer L.
                                                        Preeti
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alignment_block:
US-09-975-308-9 x US-08-988-876-2
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; CLONE: 364702
US-08-988-876-2
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                             943
                                                                                                                                                          893
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LENGTH: 1828 base pairs
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APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YUL, HENTY
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                        843 AGAACTGCAGCCAGTCCTTGCTGGGCTGTTCCTGTCCATGTGCCTGGTCA
                                                                                                                                                                                                                                                                                                                   793 AATCTAACAGATGTCTCTATATTCCTCCTAGAAGTCTCAGGGGATCC 842
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                                                                                                52 LeuHisThrProMetTyrValPheLeuThrLeuAlaValValAspIl 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                               oGluLeuGlnGlyIleIlePheLeuPhePheLeuIleValTyrLeuValA 35
                                                                                                                                                        CGGTGCTGGGGAACCTGCTCATCATCCTGGCCATCAGCCCTGACTCCCAC 942
                                                                                                                                                                                              laPheLeuGlyAsnMetLeuIleIleIleAlaLysIleTyrSerAsnThr 51
                                                                                                                                                                                                                                                                                                                                                         AsnHisSerValValThrGluPheIleIleLeuGlyLeuThrLysLysPr 18
CGGTTTCACCTCCACCACGGTCCCCAAGATGATTGTGGACATCCAGTCTC 1042
                                 eIleCysThrThrSerIleIleProLysMetLeuGlyThrMetLeuThrS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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seq_documentation_block:
   Sequence 526, Application US/09439313
   Patent No. 6329505
                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-439-313-526
                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                     APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1192
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APPLICANT:
                                APPLICANT:
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ACAGCAGAGTCATCTCCTATGCAGGCTGCCTGACTCAGATGTCTCTCTTT
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| CTCCACCTGTGGGTCTCACCTGTCAGTTGTT...TGCTGGAGGGTACCTC 1545
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                                                   Kalos, Michael
Fanger, Gary
Retter, Mark
                                                                                                            Reed, Steven G.
                                                                                                                              Jiang Yugui
                                                                                                                                                                     Dillon, Davin C.
Mitcham, Jennifer L.
                                Solk,
                                                                                                                                                   Harlocker, Susan Louise
            Day, Craig
                                  John
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; ORGANISM: Homo sapiens US-09-439-313-526
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US-09-975-308-9 x US-09-439-313-526
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CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 526
LENGTH: 963
TYPE: DNA
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                                                                    euSerCysSerProValArgIleAsnGluValMetValTyrValAlaAsp 200
                                                                                                           CTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAAGT
                                                                                                                                            yProAsnThrIleAspHisPhePheCysGluIleProProLeuLeuAlaL 184
                                                                                                                                                                                 CTCTTTTTTTCCCCACTGCCTCTGCTGATCAAGCGGCTGGCCTTCTGCCA 506
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IleThrLeuAlaIleGly...AspPheIleLeuThrCysIleSerTyrGl
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US-08-465-980-1

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APPLICATION NUMBER: US/08/465,980
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FETTATO, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
REFERENCE/DOCKET NUMBER: 325800-446
REFERENCE/DOCKET NUMBER: 314
REFERENCE/DOCKET NUMBER: 325800-446
REFERENCE/DOCKET NUMBER: 325800-446
REFERENCE/DOCKET NUMBER: 315800-446
REFERENCE/DOCKET NUMBER: 325800-446
REFERENCE/DOCKET NUMBER: 325800-446
REFERENCE/DOCKET NUMBER: 315800-446
REFERENCE/DOCKET NUMBER: 325800-446
REFERENCE/DOCKET NUMBER: 36,134
REFERENCE/DO
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MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER. CACARDA SERVICE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904
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                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                            TYPE: nucleic acid
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ZIP: 07068
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ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
                                                                                                                                                                      TOPOLOGY:
                                           NAME/KEY:
                                                                                                                                                                                                                                                                                        LENGTH: 1474 base pairs
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274..1233
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alignment_block:
US-09-975-308-9 x US-08-465-980-1
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Percent Similarity:
1046 CAGTTGTACACCGCTTTGGAAACAGCCTTCATCCCATTGTGCGTGTTGTC
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                                                                                                                                            rSerHisLeuThrValValThrLeuTyrTyrSerProValIleTyrThrT 256
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                                                                                                                                                                                                CTGCAACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGT
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                                                                                                                                                                                                                                                                                                    TGGACGTAATGTTCATCTCCTTGTCCTATTTTCTGATAATACGAACGGTT
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Percent Identity: 31.206
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1096 ATGGGTGACATCTACCTGCTGCTCCTGTCATCATCCATCATCTA 1145

271 ValAlaAlaLeuTyrThrLeuValThrProThrLeuAsnProMetValTy 287

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seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-09-053-303-1
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                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-09-053-303-1
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                                                                                                     alignment_block:
US-09-975-308-9 x US-09-053-303-1
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Patent No. 5948890
                                                                                                                                                      Ratio:
Percent Similarity:
                                                                Align seg 1/1 to: US-09-053-303-1
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAJ70
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APPLICATION NUMBER: US 08
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1474 base pair
                                                                                                                                                                                                                                                                                                                 FEATURE
364 CTTTCCATGTATGTAGTGGCAATGTGTGGAAACTGCATCGTGGTCTTCAT 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: UZIP: 07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                               LeuIleValTyrLeuValAlaPheLeuGlyAsnMetLeuIleIleIleAl 45
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: New Jersey
                                                                                                                                                                                           Quality:
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Li, Yi
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274..1233
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                                                                                                                                                            Percent Identity:
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                                                                             1474
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seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US95-07093-1
                                                                                 seq_documentation_block:
                                               Sequence 1, Application PC/TUS9507093 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               414 CGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTCTCTGCA 463
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               APPLICANT:
                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrLeuAlaValValAspIleIleCysThrThrSerIleIleProLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGACGTAATGTTCATCTCCTTGTCCTATTTTCTGATAATACGAACGGTT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gIleAsnGluValMetValTyrValAlaAspIleThrLeuAlaIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PhePheCysGluIleProProLeuLeuAlaLeuSerCysSerProValAr 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTGCTGATCAAGCGGCCTGGCCTTCTGCCACTCCAATGTCCTCTCGCAC 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hralaLeuIleMetArgLeuThrPheCysGlyProAsnThrIleAspHis 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCAATGTGGTATATGGTCTTACTGCC...ATTCTGCTGGTCATGGGCG 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTATTGTGTCCACCAGGATGTAATGAAGTTGGCCTATGCAGACACTTT 848
                                                                                                                                                                                                                                                                                                                                   yrIle.....ArgProAlaSerSerTyrThrPheGluArgAspLysVal 270
                                                                                                                                                                                                                               ATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAATCCCATCATCTA 1145
                                                                                                                                                                                                                                                               ValAlaAlaLeuTyrThrLeuValThrProThrLeuAsnProMetValTy 287
                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCAACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..AspPheIleLeuThrCysIleSerTyrGlyPheIleIleValAlaIle
                                                                                                                                                         TGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTC
                                                                                                                                                                                           rSerPheGlnAsnArgGluMetGlnAlaGlyIleArgLysValPhe 302
Li, Yi
Rosen,
                 Soppet, Daniel R.
Li, Yi
                                                                                                                                                                      1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         513
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APPLICANT:

Craig A.

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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-07093-1
                                                                                                                                                                                                                                                                                                                                                                                                               ulignment_block:
US-09-975-308-9 x PCT-US95-07093-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 1:
                                                                           514
                                                                                                                                                  464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
   564
                                                                                                                                                                                                                          414 CGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTCTCTGCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                   364 CTTTCCATGTATGTAGTGGCAATGTGTGGAAACTGCATCGTGGTCTTCAT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                    95
                                                                                                              79
                                                                                                                                                                                     62
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                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1474 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferraro, Gregory D. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: STUART & OLSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                     tSerGlnLeuPheLeuPheThrTrpSerLeuGlyAla...GluMetValL 111
                                                                                                                                                TGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATC
                                                                                                                                                                                     hrLeuAlaValValAspIleIleCysThrThrSerIleIleProLysMet 78
                                                                                                                                                                                                                                                            aLysIleTyrSerAsnThrLeuHisThrProMetTyrValPheLeuLeuT
                                                                                                            LeuGlyThrMetLeuThrSerGluAsnThrIleSerTyrAlaGlyCysMe
                                                                                                                                                                                                                                                                                                                                      LeuIleValTyrLeuValAlaPheLeuGlyAsnMetLeuIleIleIleAl 45
                                                                         CTTGCCCTTTTCTGGTTTGATTCCCGAGAGATTAGCATTGAGGCCTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201-994-1744
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274..1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363.00
1.931
66.667
.TTTATTCATGCCCTCTCAGCCATTGAATCCACCA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/465,980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                            to: 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #1.30
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7
                                                                         563
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08671525B Patent No. 5703220
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Yamada, Tag
APPLICANT: Gantz, Ira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1046
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: June 27,
                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 ValalaalaLeuTyrThrLeuValThrProThrLeuAsnProMetValTy 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 tValMetAlaIleAlaValThrAsnSerTrpValHis......T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pc-10-
                                                                                                                                                                                     COUNTRY:
ZIP: 483
                                                                                                                                                                                                                                                      ADDRESSEE: Harness, Dickey & Pierce, P.L.C STREET: P.O. Box 828 CITY: Bloomfield Hills
                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rSerPheGlnAsnArgGluMetGlnAlaGlyIleArgLysValPhe 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yrIle.....ArgProAlaSerSerTyrThrPheGluArgAspLysVal 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuArgIleArgThrValGluGlyLysArgLysAlaPheSerThrCysSe 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGACGTAATGTTCATCTCCTTGTCCTATTTTCTGATAATACGAACGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAATCCCATCATCTA 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTTGTACACCGCTTTGGAAACAGCCTTCATCCCATTGTGCGTGTTGTC 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCACACATTGGTGGTGCTACTCGCCTTCTATGTGCCACTTATTGGCCTCT 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..AspPheIleLeuThrCysIleSerTyrGlyPheIleIleValAlaIle 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gIleAsnGluValMetValTyrValAlaAspIleThrLeuAlaIleGly. 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PhePheCysGluIleProProLeuLeuAlaLeuSerCysSerProValAr 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hrAlaLeuIleMetArgLeuThrPheCysGlyProAsnThrIleAspHis 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCAACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGT 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCAATGTGGTATATGGTCTTACTGCC...ATTCTGCTGGTCATGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCTGCTGATCAAGCGGCTGGCCTTCTGCCACTCCAATGTCCTCTCGCAC 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HisTyrSerThrIleMetAsnHisHisMetCysValAlaLeuLeuSerMe 144
                                                                                                                                                                                          48303
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                                                                                                                                                                                                             SD
                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada, Tadataka
                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                       Genes Encoding Melanocortin Receptors 23
US/08/671,525B
7, 1996
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NAME/KEY:
LOCATION:
US-08-671-525B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality: 185.00
Ratio: 1.156
Percent Similarity: 49.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-975-308-9 x US-08-671-525B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1080 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-671-525B-5 from: 1 to: 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SMILT, DEALN F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-000853DVB
REFERENCE/FOOLKET NUMBER: 2115-000853DVB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810)641-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||:::::||| ||||:::||||:::|||| :::
261 CGTCAGTCTGCTGGAAAACATCCTGGTTATCCTGGCCGTGGTCAGGAACG 310
                                                                                                                                                                                                                                                                                             361 GACATGCTGGTAAGTGTGTCCAATGCCCTGGAGACCATCATGATCGCCAT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 uvalAlaPheLeuGlyAsnMetLeuIleIleIleAlaLysIleTyrSerA 50
                                                                                                                                                                    505 ATCTGCAACCTCCTGGCCATCGCCGTCGACGGTACGTCACCATCTTTA 554
                                                                                                        ::|||||:::||| :::|||||||::: :::
555 CGCGCTCCGCTACCACATCATGACCGTGAGGAAGGCCCTCACCTTGA 604
                                                                                                                                    605 TCGTGGCCATCTGGGTCTGCTGCGGCGTCTGTGGCGTGGTGTTCATCGTC 654
                                                                                                                                                                                                                                                   94 ysMetSerGlnLeuPhe.....LeuPheThrTrpSerLeuGlyAlaGlu 108
                                                                                                                                                                                                                                                                                                                                                                                      AspilelleCysThrThrSer......1lelleProLy 77
                                                                                                                                                                                                                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 325
Gaps: 12
Percent Identity: 22.154
....MetCysValAlaLeuLeuSerMetVa 145
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IMETAIAIIEAIAVAITHRASNSETTEPVAIHISTHRAIALEUILEMETA III	293 uMetGlnAla	277 LeuValThrf ::: ::: 976 ATGTGCAACT						227 ThrValGluG	869 TCTGCTGGGC	210 euThrCysIl	819 ATGCATGAAG	193 uValMetVal	778 GCACTGCCAC	177 GluIleProPa	755 GGCTG	162 rgLeuThrPhe	705 CATGATGCTCC	145 lMetAlaileA	
		roThrLeuAsnProMetValTyrSerPheGlnAsnAr ::::::::::::::::::::::::::::::::::::	CCTGGTCCTC	rThrPheGluArgAspLysValValAlaAlaLeuTyr	::: AACCCCTACTGCATCTGCTACACTGCCC	LeuTyrTyrSerProValIleTyrThrTyrIleArgP	ACCTGCCCACC	lyLysArgLysAlapheSerThrCysSerSerHisLe	CCCTTCTTCCTCCACCTGGTCCTCATCATC	≥SerTyrGlyPheIleIleValAlaIleLeuArgIle <i>l</i>	GGGCAGTCACCATCACCATTCTCCTGGGCGTGTTCA	yrValAlaAspIleThrLeuAlaIleGlyAspPheIl::::::::::::::::::::::::::::::::::::	T	oLeuLeuAlaLeuSerCysSerProValArgIleAsn	CACGTCAAGCGCATAG	CysGlyProAsnThrIleAspHisPhePheC	TCATGGGCACCCTCTACGTGCACATGTTCCTCTTTGC	laValThrAsnSerTrpValHisThrAlaLeuIleMe	

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gb_ro:AY073073
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9b_ro:AY073125

9b_ro:AY073128

9b_ro:AY074052

9b_ro:AY073124

9b_ro:AY073124

9b_ro:AY073154

9b_ro:AY0731578

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gb_pat:AX241862
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Query length: 307
Database: GenEmbl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_ro:AY073135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database sequences: 1797656
Database length: 1873333701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
Query: US-09-975-308-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MODEL-frame+_p2n.model -DEV-xlh
-Q-/cgn2_1/USPTO_spool/USO9975308/runat_24062002_090303_26237/app_query.fasta_1.368
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-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -YGAPOP=110.000 -YGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
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-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of: US-09-975-308-9 to: GenEmbl:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl:*
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5.3e-62
5.3e-63
9.9e-58
5.2e-55
9.6e-57
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                                                                                                                                                                                                                                                       5.2e-71
1.7e-70
7.1e-70
7.1e-70
7.4e-69
9.7e-68
6.4e-68
6.4e-68
9.3e-68
6.5e-67
1.6e-67
1.7e-64
1.7e-64
1.1e-66
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3.6e-66
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4.5e-74
2.2e-75
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3.3e-71
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AV073124 Mus musculus olfactory
AV073125 Mus musculus olfactory
AV073125 Mus musculus olfactory
AV073126 Mus musculus olfactory
AV073127 Mus musculus olfactory
AV073128 Mus musculus olfactory
AV073128 Mus musculus olfactory
AV073124 Mus musculus olfactory
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AY074180 Mus musculus olfactory
AY074180 Mus musculus olfactory
AY074180 Mus musculus olfactory
AY074180 Mus musculus orvegicus of
AY073132 Mus musculus olfactory
AY073176 Mus musculus olfactory
AY073176 Mus musculus olfactory
AY073062 Mus musculus olfactory
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                                                                                                                                                                                                                                                                                                                                                                                                                                       3 i AC094493 Rattus norvegicus of AV073127 Mus musculus olfactory i AV073133 Mus musculus olfactory i AX207662 Sequence 30 from Pate i AC011879 Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY073900 Mus musculus olfactory
AX350633 Sequence 11 from Paten
AX350675 Sequence 53 from Paten
                                                1 AC094493 Rattus norvegicus
AY073577 Mus musculus olfactor
AY073073 Mus musculus olfactor
                                                                                                                           AY073578 Mus musculus olfactor
AY073134 Mus musculus olfactor
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                             AC108568 Rattus
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AUTHORS
                                                                           BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
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SOURCE
ORGANISM
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LOCUS AC091612
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                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, 1 unordered pieces.
AC091612.4 GI:18497169
AC091612.4 GI:18497169
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center Code: UWGC

Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Contact: nwgchtgs@u.washington.edu
Contact: project Information
Center project name: chr-1
Center project name: RP11-656022 (sc0182)
Center clone name: RP11-656022 (sc0182)
Contact 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaul, R.K., Olson, M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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180657 bp DNA linear HTG 05
HOMO sapiens chromosome 1 clone RP11-656022, WORKING DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of I contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
    52363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 180657)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 8.4x in Q20 bases; agarose-fp Quality coverage: 9.0x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.99319
Consensus quality: 180536 bases at least 040
Consensus quality: 180650 bases at least 030
Consensus quality: 180657 bases at least 020
Consensus quality: 180657 bases at least 020
Insert size: 194815; 11.0% error; agarose-fp
Insert size: 180657; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; L08752 Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: University of Washington Genome Center
    ø
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                                   /note-
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                       /clone="RP11-656022"
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"assembly_name:Contig19"
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9.7e-56
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1.6e-55
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alignment_scores:
Quality: 1575.00
Patio: 5.130
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US-09-975-308-9 \times AC091612/rev
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Percent Similarity: 100.000
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                                                                                                                                                   ACCACCATATGTGTGTAGCCTTGCTCAGCATGGTCATGGCTATTGCAGTC
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                                                                              TATCATTGTTGCTATTCTCCGTATCCGCACAGTAGAAGGCAAGAGGAAGG
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                                         CCTTCTCAACATGCTCATCTCATCTCACAGTGGTGACCCTTTACTATTCT
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LOCUS AX241862
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Sequence 610 from Patent
AX241862
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synthetic construct
artificial sequence.
1 (bases 1 to 921)
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Bellenson, J., Smith, D.,
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COMMENT

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VERSION
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LOCUS AC026038
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             2 (bases 1 to 138591)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                       Homo sapiens chromosome 1 clone SEQUENCE, 22 unordered pieces.
Submitted (19-MAR-2000) Genome Sequencing Center, Washington
                                                           Unpublished
                                                                        The sequence of Homo sapiens
                                                                                       1 (bases 1 to 138591)
Waterston, R.H.
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                 Homo sapiens
                                                                                                                                                               human.
                                                                                                                                                                           AC026038.4 GI:9958133
HTG; HTGS_PHASE1; HTGS_
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DRAFT
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Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 129539 bases at least 040
Consensus quality: 131919 bases at least 030
Consensus quality: 133199 bases at least 020
Insert size: 140000; agarose-fp
Insert size: 140000; agarose-fp
Quality coverage: 3.88 in 020 bases; agarose-fp
Quality coverage: 4.04 in 020 bases; sum-of-contigs
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On Sep 1, 2000 this sequence version replaced qi:8567954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13;
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Center code: WUGSC
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13773 gap of
18721 contig
18821 gap of
24023 contig
24123 gap of
29088 gap of
29088 gap of
34271 gap of
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13773: gap of
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5321: gap of
9571: contig
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of 6718
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of 4002
                                                                                                                                                                                                                                                                                                                   of 9526 bp in length
unknown length
of 18721 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length of 10911 bp in
                                              of 1886
                                                                                                                                       of 2079
                                                                                                                                                                                                                                                                                                                                                                                                            of 9828
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FEATURES
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ORIGIN
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US-09-975-308-9 x AC026038
                                                                                                                                                                  alignment_scores:
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Ratio: 5.127
Percent Similarity: 100.000
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135529
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9 138591: contig of 3063
Location/Qualifiers
1. .138591
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Gaps:
Percent Identity:
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301 87686	87586 284 87636	753 26	25	23	217 87436	201 87386	184 87336	167 87286	151 87236	134 37186	117 37136	101	84 7036	67 6986	51 6936	34 6886	17 6836
1 ValPhcAlaPhcLeuLysHis 307 	AGACAAGGTGGTAGCTGCACCACTATACCACCACAAGGTGGTAGAAGGTGGTAGAAGAAGAAGAAAGA	CCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATIIGAAAG 0,000 GASpLysValValAlaAlaLeuTyrThrLeuValThrProThrLeuAsnP 284 [ProValIleTyrThrTyrIleArgProAlaSerSerTyrT	laPheSerThrCysSerSerHisLeuThrValValThrLeuTyrTyrSer 250	ellellevalalaileLeuargileargThrvalGluGlyLysargLysa 234 	ILEThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTyrGlyPh 217 	euSerCysSerProValArgIleAsnGluValMetValTyrValAlaAsp 200 	yProAsnThrIleAspHisPhePheCysGluIleProProLeuLeuAlaL 184 	ThrasnSerTrpValHisThralaLeuIleMetArgLeuThrPheCysGl 167	snhisHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaVal 150 	rAspArgTyrValAlaIleCysPheProLeuHisTyrSerThrIleMetA 134 	PheThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMetAlaTy 117 	hrSerGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeuPheLeu 100 	pileileCysThrThrSerileIleProLysMetLeuGlyThrMetLeuT 84 	ThrLeuHisThrProMetTyrValPheLeuLeuThrLeuAlaValValAs 67	alAlaPheLeuGlyAsnMetLeuIleIleIleAlaLysIleTyrSerAsn 50 	SPTOGluLeuGlnGlyIleIlePheLeuPhePheLeuIleValTyrLeuV 34

length

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VERSION
KEYWORDS
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LOCUS AL357039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 183408 bases at least Q40 Consensus quality: 186557 bases at least Q30 Consensus quality: 186087 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestesanger.ac.uk
On Aug 12, 2000_this sequence version replaced gi:9214044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 189189; sum-of-contigs
Insert size: 188721; 6.6% error; agarose-fp
Quality coverage: 4.17x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
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Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coverage: 4.30x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: bA634B7
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                   100 bp 100 bp 100 bp 100 bp 100 bp 100021 133564; contia of 11304 bp 100021 133564; contia of 100 bp 100021 133564; contia of 100 bp 100021 13564; contia of 100 bp 100021 13564; contia of 100 bp 100021 13564; contia of 100021 13564; contia of 100021 13565
133565 133664: gap of 100 bp
133665 137940: contig of 4276 bp in length
137941 138040: gap of 100 bp
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12043 12142: gap of 100 bp
12143 30262: contig of 18120 bp in length
30263 30362: gap of 100 bp
30363 41425: contig of 1063 bp in length
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18352 48451: q
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8451: gap of 100 bp
57808: contig of 9357 bp
7908: gan of
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                                                                   ap of 100 bp
contig of 27544 bp in length
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SEQUENCING IN
    alignment_scores:
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141487 143513:
143514 143613:
143614 159175
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174410 174509: (
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0 190889: contig of 16380 bp in length
coation/qualifiers
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fragment_chain:5"
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143513: contig of 2027 bp in length
43613: gap of 100 bp
159175: contig of 15562 bp in length
59275: gap of 100 bp
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                                                                                                                                                                                                              rAspArgTyrValAlaIleCysPheProLeuHisTyrSerThrIleMetA 134
                                                                                                                           ThrAsnSerTrpValHisThrAlaLeuIleMetArgLeuThrPheCysG1 167
                                                                                             eIleIleValAlaIleLeuArgIleArgThrValGluGlyLysArgLysA 234
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RKS MIZNYD M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Banks,T., Barbaria,J., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Bonnin,D., Bouck,J., Benchon,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bontok,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowte,T., Charve,M., Bryant,N.P., Burky,C., Borrell,K.L., Byrd,N.C., Carrion,T.F., Carter,M. Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,R., Checko,J., Chavez,D., Chen,G., Chen,R., Chen,R., Davila,M.L., Davis,C., Coyle,M.D., Dathorne,S.R., Davila,R.L., Davila,M.L., Davis,C., Cayaroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Day-Carroll,J.L., Dederich,D.A., Delaney,K.R., Delgado,O., Dayararoll,D., Dethorne,S.R., Davila,M.L., Davis,C., Chen,R., Chen,R., Checko,J., Charves,L., Davila,M.L., Davis,C., Chen,R., Chen,R., Checko,J., Chen,R., Chen,R., Chen,R., Chen,R., Chen,R., Davila,M.L., Davis,C., Chen,R., Chen,R., Davila,M.L., Davis,C., Chen,R., Chen,R.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                        Unpublished
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Worley,K.C. Direct Submission Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One

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COMMENT
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On Dec
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NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 127493 bases at least Q40 Consensus quality: 137458 bases at least Q30 Consensus quality: 144882 bases at least Q20 Estimated insert size: 129461; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
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----- Summary Statistics
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US-09-975-308-9 x AC094718/rev
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                                                                                                                                   eIleIleValAlaIleLeuArgIleArgThrValGluGlyLysArgLysA 234
gAspLysValValAlaAlaLeuTyrThrLeuValThrProThrLeuAsnP 284
                                     CCTGTAATCTACACCTACATTCGACCTGCATCCAGCTATACCTTTGAGAA 12780
                                                                                   CCTTCTCTACATGCTCATCTCACCTCATGGTGGTGTCCCTTTACTATTCT
                                                                                               laPheSerThrCysSerSerHisLeuThrValValThrLeuTyrTyrSer 250
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CE 2 (bases 1 to 221466)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Linton, L., Nusbaum, C., Chang, J., Chazaro, B., Anderson, S., Barna, N., Bastien, V., Boyuslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Callins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Choepel, Y., Colangelo, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., PitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Faro, S., Gord, S., Goyette, M., Grhham, L., Grand-Pierre, N., Ginde, S., Foode, S., Faro, S., Faro, S., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Kells, C., Laroque, K., Jones, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McLean, C., Macdonald, P., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., McMarthews, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Senaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Chenter, C., McCarthy, M., Carboek, L., Zimmer, A. and Zody, M.

Direct Submission

Direct Submission
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1 (bases 1 to 221466)
Birren, B., Linton, L., Nusbaum, C.
Mus musculus, clone RP23-240K1
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
Center project name: L17240

Center clone name: 240_K_1

Center clone name: Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Assembly program: Phrap; version 0.960731

Consensus quality: 220831 bases at least 040

Consensus quality: 221147 bases at least 030

Consensus quality: 221206 bases at least 020

Insert size: 230000; aggarose fp

Insert size: 221266; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
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Sciurognathi; Muridae; Murinae; Mus
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alignment_block:
US-09-975-308-9 x AC099601/rev
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                  PheThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMetAlaTy 117
                                                                     CATAATCTGCACTACAAGCATCATACCCAAAATGTTGGGAACTATGTTAA 193072
                                                                                                                                                                         pIleIleCysThrThrSerIleIleProLysMetLeuGlyThrMetLeuT 84
                                                                                                                                                                                                                                ThrLeuHisThrProMetTyrValPheLeuLeuThrLeuAlaValValAs 67
                                                                                                                                                                                                                                                                                                                                 alAlaPheLeuGlyAsnMetLeuIleIleIleAlaLysIleTyrSerAsn 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAACTTCAGCATTGTTAGTGAGTTTATGATTCTGGGACTTACTCAAAA 193272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetAsnHisSerValValThrGluPheIleIleLeuGlyLeuThrLysLy 17
                                                                                                                                                                                                                                                                                                           TGGCTCTACTTGGTAATATGCTAATTGTTGTTGCCATAATCTATAACACC 193172
TTCACATGGTCCTTGGGGGCTGAGATGGTGCTCTTTACTACAATGGCCTA 192972
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Ratio: 4.631
milarity: 97.386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 11.4 in Quality coverage: 11.9 in
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10012 74781; contig of 64770 bp in length
74782 74881; gap of 100 bp
74882 221466; contig of 146585 bp in length
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39922 c 39522 g
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clone_end:T7
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74882. .221466
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10012. .74781
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/db_xref="taxon:10090"
/clone="RP23-240K1"
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    snHisHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaVal
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 926)
Zhang, X. and Firestein, S.
             Submitted (11-JAN-2002) Celera Rockville, MD 20850, USA
                                            Direct Submission
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AY073900
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Location/Qualifiers
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alignment_scores:
Quality: 1354.00
Ratio: 4.544
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                                                                                               TGACCGCTATGTGGCCATTTGCTTCCCACTTCGCTATAGTACTATTATGA
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                                                                    yProAsnThrIleAspHisPhe.PheCysGluIle.ProProLeuLeuAl 183
spIleThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTyrGly 216
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internal stop codons"
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209 c 181 g 309
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US-09-975-308-9 x AX350633
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                                                                                                                                                                               Quality: 1339.00
Ratio: 5.170
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etLeuThrSerGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeu 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        798 bp
Sequence 11 from Patent W00177177.
AX350633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX350633.1 GI:18616201
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                                                                                                                                                                              gb_pat:AX350675
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Sequence 53 from 1
AX350675
Shenoy, S., Gangolli, E.A., Rastelli, L., Smithson, G., Padigaru, M., Vernet, C.A., Wolenc, A.R., Casman, S.J., Tchernev, V.T., Szekeres, E.S., Gorsse, W., Alsobrook, J.P. and Burgess, C.E. Novel gpcr-proteins and nucleic acids encoding same Patent: WO 0177177-A 53 18-OCT-2001;
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   Homo sapiens
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                                                   TyrThrPheGluArgAspLysValValAlaAlaLeuTyrThrLeuValTh 279
                                                                        CCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGC
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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Maccares, R., Landers, T., Leboczky, J., Levine, R., Liu, G.,
Maccarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Maylor, J., Myuyen, C.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Direct Submission
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-101J20
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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HTG; HTGS_PHASE0.
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Mus musculus clone RP23-101J20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse
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                                                                                                                                                                                                                                                                                               NOTE: This record contains 76 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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                                                                                                                                                                                                                                            will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: L16346
Center clone name: 101_J_20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                        preserved.
                             680 779; gap of 100 bp
780 1489; contig of 710 bp in length
1490 1589; gap of 100 bp
1590 2263; contig of 674 bp in length
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                                                                                                                                                                                                                                         is updated, the accession
                                                                                                                                                            679: contig of 679 bp in length
contig of 674 bp in length of 100 bp
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LOW-PASS SEQUENCE SAMPLING.
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murinae; Mus
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23587 24261: contig of 6
24262 24361: gap of 10
24362 25046: contig of 68
25047 25146: gap of 100
25147 2507: contig of 68
25808 25907: contig of 68
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9326 9425: gap
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16489 17234: contig of 746 bg
17235 17334: gap of 100 bp
17335 18009: contig of 675 bp
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6164:
5 6264: gap
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3839:
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22814: gap of 100 t
23486: contig of 672
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18109: gap of 100 bp
18108: contig of 693 bg
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                                                                                 29126: gap of 100 bp
29814: contig of 688 bp
29914: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                         25907: gap of 
26596: cont
30588: contig of 674 bp
30688: gap of 100 bp
31361: contig of 673 bp
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20385: contig of 677 bp 1
10485: gap of 100 bp 1
21178: contig of 693 hr
278: gap of
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1581: gap of 100 bp

13254: contig of 673 bp

13254: gap of 100 bp
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4630:
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14033: contig of 679 bp
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10127: contig of
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29026: contig of 703 bp
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1942: contig of 664 bp
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51118 51815; contig of 698
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35 39230: contig of 696 bp in 1
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33700: contig of 695 bp
33800: gap of 100 bp
34476: contig of 676 bp
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32905: contig of
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32127: con
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52639: contig of 724 bp in length
52739: gap of 100 bp
53441: contig of 702 bp in length
53541: gap of 100 bp
54230: contig of 689 bp in length
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47064: contig of 696 bp in 16
77164: gap of 100 bp
47871: contig of 707 bp in 16
7971: gap of 100 bp
48663: contig of 692 bp in 16
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436: gap of 100 bp
43096: contig of 660 bp in length
196: gap of 100 bp
43085: contig of 689 bp in length
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35272: contig of 696
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                            Submitted (11-JAN-2002) Celera Rockville, MD 20850, USA
                                                                             Adams, M.
                                                                                                                           The olfactory receptor gene superfamily of the mouse Nat. Neurosci. 5 (2), 124-133 (2002)
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 915)
                                                                                                                                                                                                                           Mus musculus
                                                            Direct Submission
                                                                                                                                                           Zhang, X. and Firestein, S.
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                                                                                                                                                                                                                                           house mouse.
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Location/Qualifiers
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Sciurognathi; Muridae;
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                                                                                            GCCCCAGAGTGTGCATTTCTGGCTGGCATTGTCTGGGCTATCAGCCTG
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ACTAACACCAGCATAAACTCAAGCCTGGTGCTACGTCTACCATTCTGCAG 497
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/db_xref="taxon:10090"
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Mus musculus olfactory receptor
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Zhang, X. and Firestein, S.
The Olfactory receptor gene superfamily of the mouse The Olfactory receptor gene superfamily of the Mouse
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                                                                                                                                                                         Submitted (11-JAN-2002) Celera Genomics, Rockville, MD 20850, USA
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/chromosome="7"
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               /evidence=not_experimental
287 c 200 g 244
                                                                                                                                 /organism="Mus musculus"
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MOR251-5 pseudogene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 GCCTCACCTTCGGGTACCTCTTCTTCAGCTTCCTCTGCCTATACATGG
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snHisHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaVal 150
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                                  ProVallleTyrThrTyrIleArgProAlaSerSerTyrThrPheGluAr 267
                                                                                         laPheSerThrCysSerSerHisLeuThrValValThrLeuTyrTyrSer
                                                                                                                                                                                                                                                      IleThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTyrGlyPh
                                                                                                                                                                               eIleIleValAlaIleLeuArgIleArgThrValGluGlyLysArgLysA 234
                                                                                                                                                                                                                     GTGTTCCTGGCTGTAGGGAACTTCTCTGTGACAATCCTCTCTATGGCTT
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                                                                                                                                             TATTGTGGCCAGCATCCTGAAGATCCGGTCAGCTGAGGGCCAAGCGACGAG
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TITLE:
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LOCUS AC094870
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                                                                                                                                                                                                                                                                                                                                                                                                                  Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buray, C., Bourch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Caracter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hallins, B., Homsi, F., Howard, S., Huber, J., Hallyk, S., Hume, J., Jackson, L.E., Jackson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Li, J., Lithtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Marince, E., Massey, E., Mawhiney, E., Martin, R., Martindale, A., Marince, E., Woken, N., Newtson, N., Nguyen, N., Nickerson, E., Nwoken, N., Payton, B., Peery, J., Peters, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Shooshtari, N., Boner, S., Scherer, S., Scott, G., Shen, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, S., Wastren, R., Washington, C., Vinson, R., Washington, C., Vinson, R., Wall, R., Wang, S., Wastren, R., Washington, C., Vinson, R., Washington, C., Vara, V., Villalon, O., Vinson, R., Wall, R., Wang, S., Wastren, R., Washington, C., Vinson, R., Wall, D., Vinson, R., Wall, D., Vinson, R., Wall, D., Vinson, R., Wall, D., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sValPheAla 303
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Worley, K.C.
Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Depa:
of Molecular and Human Genetics, Baylor College of Medicine,
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                     Unpublished
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Bark
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus clone CH230-5N18,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900
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Department

COMMENT

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Baylor Plaza, Houston, TX 77030, USA on Dec 20, 2001 this sequence version replaced gi:15624706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 96697 bases at least Q40
Consensus quality: 104847 bases at least Q30
Consensus quality: 112341 bases at least Q20
Consensus quality: 12341 bases at least Q20
Estimated insert size: 92352; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 1.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GBPG
Center clone name: CH230-5N18
-----Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor Co
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Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burcel, K.L., Byrd, N.C., Carron, T.E.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,
Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O.,
Dann, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Davis, C.,
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Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
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Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
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Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
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Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Nugyen, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N.,
Wall, R., Wang, S., Warfen, R., Washington, C.,
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Wall, R., Wang, S., Walliamson, A., Wieczyk, R., Hooden, S.,
Walls, R., Wang, S., Walliamson, A., Wieczyk, R., Hooden, S.,
Walls, R., Wang, S., Walliamson, A., Wieczyk, R., Hooden, S.,
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Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:17062158.
                                                                                                                                                    Worley, K.C.
Direct Submission
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Barbaria,J.,
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findPhrapList

Assembly program:

Summary Statistics

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14083 14183 18912 19012 22085 22185 26200 26300 28569 28669 31740 337777

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 96 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 163315 bases at least Q40 Consensus quality: 177813 bases at least Q30 Consensus quality: 189359 bases at least Q30 Estimated insert size: 163704; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 1.8x in Q20 bases; sum-of-contigs estimation
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Center project name: GBEW
Center clone name: CH230-5F7
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Center code: EDM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
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roMetValTyrSerPheGlnAsnArgGluMetGlnAlaGlyIleArgLys 300
                                                                                                                                                                                                                                                                     laPheSerThrCysSerSerHisLeuThrValValThrLeuTyrTyrSer 250
                                                                                                                                                                                                                                                                                                                                                                                 eIleIleValAlaIleLeuArgIleArgThrValGluGlyLysArgLysA 234
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                                                                                                                                                                   ProVallleTyrThrTyrIleArgProAlaSerSerTyrThrPheGluAr 267
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                                                                                                                                                                                                                                                                                                                                                               RES ALSONO, D. M. Addio-Oduola, B. Ali-osman, F.R., Allen, C. Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Barboroks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTCATCTACACTCTGAGGAACAAAGATGTCAAAGTTGCACTCCGGAAA 95850
                                                            Submitted (17-SEP-2001) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15628089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204143 bp D
Rattus norvegicus clone CH230-58J17,
***, 62 unordered pieces.
AC096461
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NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project Information
Center project name: GFXC
Center clone name: CH230-58J17
Center clone name: CH230-58J17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
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Align seg 1/1 to: AC096461 from: 1 to: 204143 59236 CAAATTGGCTGGTGTGCTGTATACCATGCTGAGCCCCACGCTCAACCCTC 59285 59186 59286 TGATCTACACTTTGAGAAACAAGGAGGTCAAGGCAGCTCTCAGGAAAATT 59335 59136 58986 58836 AAGCATTTTGCGGCGTGCTGGCTGGTGTGTGCGCGCTTTGTGCTTTC 58885 58786 58736 ACATGGTCTGCTTCCTCAGAGTTGCTCCTCCTCACTGTCATGGCCTACGA 58785 58686 AGAGAAACCCTATCTCCTATGGTGGCTGCATGACCCAGCTCTATTTCCTT 58735 58636 CATCTGTACCTCCTCCATTATGCCAAAGGCCCCTGAAGGGTCTGGTGTCAA 58685 58536 CCCTCTCAGGTAATGTCCTTATCATCTTGGCCATCACCTGCAACCCTGGG 58585 58486 GCAGTACCAGCTGCTCTTATCTGTTTCCTCTCTCTCTACTGCGTGG 58535 185 285 etValTyrSerPheGlnAsnArgGluMetGlnAlaGlyIleArgLysVal 301 252 135 isHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaValThr 151 102 ThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMetAlaTyrAs 118 85 erGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeuPheLeuPhe 101 35 laPheLeuGlyAsnMetLeuIleIleIleAlaLysIleTyrSerAsnThr 18 oGluLeuGlnGlyIleIlePheLeuPhePheLeuIleValTyrLeuValA 35 ValileTyrThrTyrIleArgProAlaSerSerTyrThrPheGluArgas 268
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GTCTTTTATGCCTACATAAGCCCTGTCTCCAGCTATAACGCAGAGAAGAG 59235 CCTGTAGCTCCACCTATGTGAACAGTGTCATGATTGTCTTGGCTGACGCC 59035 erCysSerProValArgIleAsnGluValMetValTyrValAlaAspIle 201 TTTTATGGCATATTGAACTTCCTGATGACCATCGTGTCGTATGGCTTCAT 59085 58485 85

302 PheAlaPheLeuLysHis 307
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59336 TTCCCTTTTCTCAGAAAT 59353

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Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
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Query length: 307
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-Q-/cgn2_1/USPTO_spool_US09975308/runat_24062002_090304_26270/app_query.fasta_1.368
-Q-/cgn2_1/USPTO_spool_US09975308/runat_24062002_090304_26270/app_query.fasta_1.368
-DB=N_geneseq_032802 -QEMPU-fastap -SUFFIX=rng -GAPOD=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -GAPEXT=7.000 -XGAPOD=10.000 -YGAPEXT=0.500
-GAPEXT=0.000 -GAPEXT=7.000 -YGAPOD=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -TRR_SCORE=pct
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -TRR_SCORE=pct
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -TRR_SCORE=pct
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -TRR_SCORE=pct
-TRANS=100 -TRR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09975308_@CGN1_1_0 -NCPU=6 -ICPU=3 -LONGLOG
-TORNS=START=1 - ALIGN=15 -NCPU=6 -ICPU=3 -LONGLOG
-TORNS=START=1 - ALIGN=15 -NCPU=6 -ICPU=3 -LONGLOG
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+ 725.00 1331.47 8.1e-66

+ 723.00 1297.98 6.0e-64

+ 707.00 1296.63 7.1e-64

+ 706.00 1296.08 7.6e-64

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+ 706.00 1295.84 4.3e-63

+ 699.00 1282.80 4.2e-63

+ 693.00 1275.52 1.1e-62

+ 693.00 1271.76 1.7e-62

+ 691.00 1268.06 2.8e-62

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Align seg 1/1

to: AAH32037

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1 MetAsnHisSerValValThrGluPheIleIleLeuGlyLeuThrLysLy 17

Percent Similarity:

Quality: 1574.00 Ratio: 5.127 nilarity: 100.000

Percent Identity:

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seq_documentation_block:
ID AAH32037 standard:
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A. DAT: AAK28297
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A. DAT: AAX12821
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A. DAT: AA112861
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A. DAT: AA134218
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A. DAT: AA102777
                                         The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties
                                                                                                                                                                                                                                                                                                                 New polynucleotides which sensation for identifying
                                                                                                                                                                                                                                                                                                                                                                     WPI;
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24-FEB-2000; 2000US-0184809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; olfactory receptor; OR; primary scent determinati
secondary scent determination; polypeptide library; odou
scent profile; scent fingerprint; scent representation;
Sequence 921 BP; 218
                                of different individuals.
                                                                                                                                                                                                                                                                                   Claim
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(YEDA ) YEDA RES & DEV CO LTD
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olfactory agonists and antagonists
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ValPheAlaPheLeuLysHis
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AAS42323

Align seg 1/1

to: AAS42323

from:

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alignment_scores:

Ratio: Similarity:

Quality: 1574.00 Ratio: 5.127 nilarity: 100.000

Percent

Identity:

99

Length:

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAS42323
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24-MAR-2000; 2000US-0192033.
12-APR-2000; 2000US-0198474.
24-APR-2000; 2000US-019935.
26-MAY-2000; 2000US-0207702.
23-JUN-2000; 2000US-0213849.
16-AUG-2000; 2000US-0226534.
07-SEB-2000; 2000US-0236534.
07-FEB-2001; 2001US-0266862.
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ss; food additive; cosmetic
                                                                                  The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific specific specific specific specific specific specific specifically recognise molecules, odourants, that elicit specific specif
                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human olfactory 6 protein-coupled receptors, useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customise odours
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 135; 319pp; English.
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                                                                                                            ProValIleTyrThrTyrIleArgProAlaSerSerTyrThrPheGluAr
                                                                                                                                                           laPheSerThrCysSerSerHisLeuThrValValThrLeuTyrTyrSer
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901 GTGTTTGCATTTCTGAAACAC 921

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:AAS17179

cDNA; 798 ВP

(first entry)

a novel G protein-coupled receptor, NOV6

Human; ss; G protein-coupled receptor; GPCR; NOV6; cardiant; antiarteriosclerosis; antibacterial; virucide; fungicide; protozoacide; antidiabetic; cytotoxic; analgesic; antiasthmatic; nootropic; neuroprotective; antiinflammatory; gene therapy; transgenic animal; cardiomyopathy; atherosclerosis; infection; pain; anorexia; bulimia; asthma; neurological disorder; Parkinson's disease; stroke; Alzheimer's disease; multiple sclerosis; lesional psoriatic skin; ischaemia; cirrhotic hepatitis; acute pancreatitis; diabetes; cancer; angiogenesis; obesity; olfactory disorder; chromosome 11.

seq_documentation_block:
ID AAS17179 standard; cD
XC AAS17179;
XC AAS17179;
XC AAS17179;
XX Id-FEB-2002 (first e
XX Human; ss; G proteinKW Human; ss; G proteinKW Antiarteriosclerosis;
KW antiarteriosclerosis;
KW antiarteriosclerosis;
KW antiarteriosclerosis;
KW Human; ss; G proteinKW Human; ss; G proteinKW Human; ss; G proteinKW Alzheimer; s disease;
KW cardiomyopathy; ather
KW asthma; neurological
KW Alzheimer; s disease;
KW angiogenesis; obesity
CS; Homo sapiens.

KW Alzheimer; s disease;
KW angiogenesis; obesity
CS; Homo sapiens.

KW Alzheimer; s disease;
KW angiogenesis; obesity
CS; Homo sapiens.

KW Alzheimer; s disease;
Locat
FH Key
Il-APR-2000; 2000US-1
PR 11-APR-2000; 2000US-1
PR 21-APR-2000; 2000US-1
PR 21-APR-2001; 2001US-2
PR 21-JUL-2000; 2000US-1
PR 21-APR-2001; 2001US-1
PR 21-APR-2001; 2 /*tag= 24..782 /product=783..798 Location/Qualifiers 1..23 /*tag-/*tag= ь D a "NOV6"

2001WO-US11901

2000US-199964P 2000US-199948P 2000US-199956P 2000US-199956P 2000US-200176P 2000US-218995P 2000US-220644P 2001US-254861P 2001US-264851P 2001US-268567P 2001US-0220644 2000US-195994P 2000US-196538P

(CURA-) CURAGEN CORP.

Alsobrook EAG, AR, k JP, Rastelli L, Smithson G, Casman SJ, Tchernev VT, Burgess CE; Padigaru M, Szekeres ES,

Human G-protein coupled receptors, NOV1-12, useful for diagnosis treatment of e.g. cardiomyopathy, also in screening for specific modulators and

30; 171pp; English

The invention relates to Human G-protein coupled receptor (GPCR) polypeptides, designated NOV1-12, nucleic acids encoding them,

301

ValPheAlaPheLeuLysHis

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cc variants of them, a vector containing the nucleic acid, a host cell containing the vector, a method for identifying modulators of the GPCRs cc and antibodies raised against them. The NOVI-12 polypeptides and nucleic cc acids are used to identify ligands and antyagonists, they are also used to diagnose and treat GPCR-associated diseases, e.g. cardiomyopathy, cc atherosclerosis, diseases related to cell-signalling or metabolic contains, but and antyagonists, they are also used contained to early signal and antyagonists, they are also used contained to the signal ling or metabolic contains and the signal in the signal ling or metabolic contains and setting and contained participation. The partitis, acute pancreatitis, contained to signal and contained and signal contained and signal and contained and signal and contained and signal and contained and signal and signal and contained and signal and sign
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tAlaTyrAspArgTyrValAlaIleCysPheProLeuHisTyrSerThrI 132
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                                                                                                     GCTGATATTACCCTGGCCATAGGGGACTTTATTCTTACCTGCATCTCCTA
                                                                                                                              AlaAspIleThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTy
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Ratio: 5.170
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                                                                                                                                                                                                                                                                                                                                                                                                                       Human; olfactory receptor; G
ss; food additive; cosmetic;
 The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of
                                                                                               Nucleic acids encoding human olfactory G protein-coupled receptors, useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customise odours -
                                                                                                                                                                                                                                                                                                                                     13-MAR-2001; 2001WO-US07771
                                                                           Claim 1; Page 117; 319pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eGluArgAspLysValValAlaAlaLeuTyrThrLeuValThrProThrL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA encoding olfactory receptor AOLFR81
                                                                                                                                                                                                                            ; 2000US-0188914.

; 2000US-0192033.

; 2000US-0198474.

; 2000US-0199335.

; 2000US-0207702.

; 2000US-021849.

; 2000US-0226534.

; 2000US-0266862.
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fragrance; pharmaceutical
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their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and fragrances. The present sequence encodes a human olfactory receptor of

the invention.

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                                                                                                erCysSerProValArgIleAsnGluValMetValTyrValAlaAspIle
                                                                                                                              AACACGGCCATCCACACGGGGCTGATGCTGCGCTTGGATTTCTGTGGCCC
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Similarity:
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                                                                                  CCTGCAGCTCCACCTACGTCAACGGTGTCATGATTGTCCTGGCGGATGCT
                                                                                                                                                                                                                              AGGTGTTCTGCAGCGGGCTGGCCACAGCCGTGTGGCTGCTCTGCGCCGTC
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                                    TTCTACGGCATAGTGAACTTCCTGATGACCATCGCGTCCTATGGCTTCAT
                                                                                                                                                                                                     AsnSerTrpValHisThrAlaLeuIleMetArgLeuThrPheCysGlyPr
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seq_documentation_block:
ID AAD12952 standard; ccl
AC AAD12952;
XX AC AAD12952;
XX 16-OCT-2001 (first e
XX Human; G-protein coupl
XX Homo sapiens.
XX Howel 150000; 200005-
XX Howel 150146 human
PT Protein ing and treat
PT disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide; antiinflammatory; anticonvulsant; antiemette; neuroprotective; nootropic; cerebroprotective; hypotensive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; Huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia; anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder; Addison's disease; Crohn's disease; acquired immune deficiency syndrome; AlDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity; osteoporosis; transgenic animal; gene therapy; ss.
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/product-

2000US-0180093 2000US-0182045

01-FEB-2001; 2001WO-US03455

(INCY-) INCYTE GENOMICS INC

Au-Young Ţ

2001-488869/53. DB; AAE06759.

Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metaboli and metabolic

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alignment_block: us-09-975-308-9 \times AAD12952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is human G-protein coupled receptor-9 (GCREC-9) cDNA. The present invention relates to GCREC protein and nucleic acids encoding them. GCREC protein, its agonist or antagonist are useful for treating diseases or conditions associated with decreased expression or overexpression of functional GCREC in a pattent, where the disorder is selected from cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and cancer, neurological disorders such as epilepsy, stroke, Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as hypertension, vasculitis, varicose veins, gastro-
intestinal disorders such as dysphagia, dyspepsia, anorexia, nausea,
pancreatitis, autoimmune/inflammatory disorders such as acquired
immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease,
uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic
infections, trauma and metabolic disorders such as diabetes, obesity,
osteoporrosis. GCREC proteins and their cDNAs are used to assess the
effects of exogenous compounds on the expression of GCREC sequences.
GCREC cDNA is useful to create knock in humanised animals (pigs) or
transgenic animals (mice or rats) to model human disease, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic or diagnostic purposes, for somatic or germline gene therapy, to generate hybridisation probes useful in mapping the naturally occurring genomic sequence, and in molecular biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, Huntington's disease, Parkinson's disease, cardiovascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 AACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCC
135 isHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaValThr 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 oGluLeuGlnGlyIleIlePheLeuPhePheLeuIleValTyrLeuValA 35
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                                                                                                                                             eIleCysThrThrSerIleIleProLysMetLeuGlyThrMetLeuThrS
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                                                                                         pArgTyrValAlaIleCysPheProLeuHisTyrSerThrIleMetAsnH 135
                                                                                                                                                                                                                                                 erGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeuPheLeuPhe 101
                                                                                                                                                                                                                                                                                                                                                       CCGGTACGCAGCCATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCA 720
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Gaps:
Percent Identity: '
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seq_documentation_block:
ID AAH31706 standard; DNA; 924 BP
XX
AC AAH31706;
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DT 30-JUL-2001 (first entry)
XX
Human olfactory receptor polyn
XX
Human; olfactory receptor; OR;
XX
secondary scent determination;
XX
secont profile; scent fingerpri
XX
Homo sapiens.
XX
PN W0200127158-A2.
XX
PD 19-APR-2001.
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PD 19-APR-2001.
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PD 20-OCT-1999; 99US-0158615.
PR 24-FEB-2000; 2000US-0184809.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD
XX
PI Bellenson J, Smith D, Lancet
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                                                                                                                                                                                                                                                                                Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds.
                                                                                                                                                                                                                                                                                                                                                      Human olfactory receptor polynucleotide, SEQ ID
                                      (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAH31706
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Lancet D,

Glusman

Fuchs

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alignment_scores
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AsnSerTrpValHisThrAlaLeuIleMetArgLeuThrPheCysGlyPr 168
                                                                    isHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaValThr 151
                                                                                                                                 pArgTyrValAlaIleCysPheProLeuHisTyrSerThrIleMetAsnH 135
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                                       AGGTGTTCTGCAGCGGGCTGGCCACAGCCGTGTGGCTGCTCTGCGCCGTC
                                                                                                              CCGGTACGCAGCCATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCA
                                                                                                                                                                                      ACGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGA
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seq_documentation_block:
ID AAS42455 standard;
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                                                                                          12-APR-2000;
24-APR-2000;
                                                                                                                   13-MAR-2000;
24-MAR-2000;
                                                                                                                                                      13-MAR-2001;
                                                                                                                                                                                                      WO200168805-A2
                                                                                                                                                                                                                                                                                       Human cDNA encoding olfactory receptor AOLFR130B
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16-AUG-2000; 07-SEP-2000; 26-MAY-2000; 23-JUN-2000;

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US-09-975-308-9 x AAS42455
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific specifically recognise molecules, odourants, that elicit specific encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and pharmaces. The present sequence encodes a human olfactory receptor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding human olfactory G protein coupled receptors, useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customise odours -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 194; 319pp; English.
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                           isHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaValThr
                                                           ThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMetAlaTyrAs 118
                                                                                                                                                                                            AGAAGAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTGCATTC
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seq_documentation_block:
ID AAF61132 standard; cD
XX AAF61132;
XC AAF61132;
XX 17-MAY-2001 (first e
XX OLFXY; gene therapy;
XX OLFXY; gene therapy;
XX Human OLFXY cDNA.
XX CDS Homo sapiens.

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diagnosis, treatment and development of pharmaceuticals

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US-09-975-308-9 x AAF61132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAF61132
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                                                                                                                                                                                                                                                                                                                                                                                                                        1391 CTGCTACACCACCAGCAATGTCCCCCCAGATGATGGTGCACCTCCTCTCAA
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1591 AGGTTCTATGCAATCAATTAGCAGCCTCATGCTGGGCTGCTGGTTTCCTT
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                                                                                                                                                                                                              GTTTTCTTTGTAGGATCAGAGTGTCTCCTACTGACAGCAATGGCATATGA
                                                                                                                                                                                                                                                                                                                       AGAAAAAAAGCATTTCTTATGTGGGGTGTGTGGTTCAACTTTTTGCATTT 1490
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                                                isHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaValThr 151
                                                                                                                                                                                                                                                               ThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMetAlaTyrAs 118
                                                                                                                                                         pArgTyrValAlaIleCysPheProLeuHisTyrSerThrIleMetAsnH 135
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235
                            New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -
                                                                                                           Bellenson J,
                                                                                                                                                                                        08-OCT-1999; 99US-0158615
24-FEB-2000; 2000US-0184809
                                                                                                                                                                                                                                                                       19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                   Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH31995 standard; DNA;
                                                                             WPI; 2001-290713/30
                                                                                                                                        (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                        06-OCT-2000; 2000WO-US27582
                                                                                                                                                                                                                                                                                                       WO200127158-A2
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Human olfactory receptor polynucleotide,
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                                                                                                           Smith D,
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                                                                                                           Lancet D,
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Claim 8; Page 407; 1857pp; English.

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alignment_block:
US-09-975-308-9 x AAH31995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCACACACCCATGTATTTTTTCCTCTGCAACCTCTTCTTTGACCT
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                                                                                                                                                                                                                                                          pargTyrValAlaIleCysPheProLeuHisTyrSerThrIleMetAsnH 135
                                                                                                                                                                                                                                                                                                                           ThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMetAlaTyrAs 118
                                                                                                                                                                                                                                                                                                                                                                            ATCACAAAGTTATCTCCTTCTCCAGCTGTGCCACCCAGTTTGCTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                             erGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeuPheLeuPhe 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCTACTCCTCAGCCATTGCCCCCAGGATGCTGGCTGACTTCCTAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elleCysThrThrSerIleIleProLysMetLeuGlyThrMetLeuThrS
GTAGGTTTTGTGGATGCTGAGTGCTATGTCCTGGCAGCCATGGCCTATGG
                                                                        AGTTTAGTAGCCCACACTACCCTCACCTTCAGCCTGAGTTACTGTGGTTC
                                                                                                          AsnSerTrpValHisThrAlaLeuIleMetArgLeuThrPheCysGlyPr 168
                                                                                                                                               isHisMetCysValAlaLeuLeuSerMetValMetAlaIleAlaValThr 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human olfactory receptor polynucleotide, SEQ
 The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour secondary scents and the identification of combinations of odour
                                                                                                                                                                                                                                                                        08-OCT-1999; 99US-0158615
24-FEB-2000; 2000US-0184809
                                                                                                                                                                                                                                 (DIGI-) DIGISCENTS.
(YEDA ) YEDA RES & DEV
                                                                                                                                                                                                                                                                                                                 06-OCT-2000; 2000WO-US27582
                                                                                                                                                   New polynucleotides which
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scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory facultles

individuals

The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary

Claim

8; Page 437; 1857pp; English.

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH32067
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    AAH32067 standard;
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CCTTCAGCACCTGCTCCCCACCTTACAGTGGTGATTATATTCTATGGC
               laPheSerThrCysSerSerHisLeuThrValValThrLeuTyrTyrSer
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                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human olfactory G protein-coupled receptors, useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customise odours -
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od additive; cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SENOMYX INC
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; 2000US-0198474.
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receptors, OR, (a G protein coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and pharmaceit. The present sequence encodes a human olfactory receptor of

of.

The invention relates to nucleic acids encoding human olfactory

Claim 1; Page 173; 319pp; English.

Sox

Sequence

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                                                                    CATAACTCAAGCTGTGCTGAGGATCAAATCAGTAGAGGCAAGGCATAAAG
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CCTTCAGCACCTGCTCCCCACCTTACAGTGGTGATTATATTCTATGGC
                                                                                      GTTCTGTTTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTT
                                                                                                                                                                       IleThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTyrGlyPh
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                                        The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptor and can be used for determining differences in the olfactory faculties
                                                                                                                                                                                                                                                                                              New polynucleotides which encode polypeptides involved in ol sensation for identifying olfactory agonists and antagonists
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24-FEB-2000; 2000US-0184809
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Sequence 927

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alignment_block: US-09-975-308-9 \times AAH32033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sLysProGluLeuGlnGlyIleIlePheLeuPhePheLeuIleValTyrL 33
                                                                                                                                                                                                                                                                                                                                                                                                                         leMetAsnHisHisMetCysValAlaLeuLeuSerMetValMetAlaIle 148
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                                                                                                                                                                                                                                                                                                                                                                   AlaValThrAsnSerTrpValHisThrAlaLeuIleMetArgLeuThrPh 165
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                        TyrSerProValIleTyrThrTyrIleArgProAlaSerSerTyrThrPh
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                                                       GCAAAGCCTTCTCCACCTGTGGTTTTTACCTCACCGTGGTGACGCTCTTT
                                                                     rgLysAlaPheSerThrCysSerSerHisLeuThrValValThrLeuTyr
                                                                                                                                          rGlyPheIleIleValAlaIleLeuArgIleArgThrValGluGlyLysA
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ID AAS42313 standard; cD
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AC Human cDNA encoding c
KW Human; olfactory rece
KW Human; olfactory cooling-
OS Homo sapiens.

XX W0200168805-A2.

XX W0200168805-A2.

XX 13-MAR-2000; 2000US-0
PR 24-MAR-2000; 2000US-0
PR 24-MAR-2000; 2000US-0
PR 24-MAR-2000; 2000US-0
PR 24-MAR-2000; 2000US-0
PR 26-MAY-2000; 2000US-0
PR 23-JUN-2000; 2000US-0
PR 23-JUN-2000; 2000US-0
PR 07-FEB-2001; 2001US-0
PR 07-FEB-2001; 2001US-0
PR 07-FEB-2001; 2001US-0
PR 07-FEB-2001; 2000US-0
PR 07-FEB-2001; 2001US-0
PR 07-FEB-2001; 2000US-0
PR 07-FEB-20
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                                                                                                The invention relates to nucleic acids encoding human olfactory receptors, OR, (a G protein coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific specifically recognise molecules, odourants, that elicit specific specific specification. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and pharmaces. The present sequence encodes a human olfactory receptor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA encoding olfactory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 130-131; 319pp; English.
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od additive; cosmetic;
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TyrSerProValIleTyrThrTyrIleArgProAlaSerSerTyrThrPh
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                                                                                                                                                                                                                                                                                                                                                                           CCTCACCTCCACTCCCTGCACACACTTCTGCTGAATCGTCTCACCTT
                                                                                                                                                                                                                                                                                                                                                                                                           AlaValThrAsnSerTrpValHisThrAlaLeuIleMetArgLeuThrPh 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATATTTGCTTTACAACAAGCGTTGTCCCCCAAGATGCTGATGAACTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euValAlaPheLeuGlyAsnMetLeuIleIleIleAlaLysIleTyrSer
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                                                                                                                                   rGlyPheIleIleValAlaIleLeuArgIleArgThrValGluGlyLysA
                                                                                                                                                                                AlaAspIleThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTy
                                                                                                                                                                                                                                                                 euAlaLeuSerCysSerProValArgIleAsnGluValMetValTyrVal 198
                                                                                                                                                                                                                                                                                                             CTGTGACTCCAATGTTATCCACCACTTTCTCTGTGACCTCAGCCCTGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                          leMetAsnHisHisMetCysValAlaLeuLeuSerMetValMetAlaIle 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euThrSerGluAsnThrIleSerTyrAlaGlyCysMetSerGlnLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCATCTTCAGACCCCTATGTATTTCTTCTTGAGTTTTCTGTCTCTCAC
                                                  GCAAAGCCTTCTCCACCTGTGGTTTTTACCTCACCGTGGTGACGCTCTTT
                                                                               rgLysAlaPheSerThrCysSerSerHisLeuThrValValThrLeuTyr
                                                                                                                TATACGAATCCTCACTACAGTTCTCAAGATTCCCTCTACTTCTGGGAAAC
                                                                                                                                                                                                                                             TGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACA
                                                                                                                                                                                                                                                                                                                                           eCysGlyProAsnThrIleAspHisPhePheCysGluIleProProLeuL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tAlaTyrAspArgTyrValAlaIleCysPheProLeuHisTyrSerThrI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuPheThrTrpSerLeuGly...AlaGluMetValLeuPheThrThrMe 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCCTCATCGTGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCTTTGACCGCTATGTGGCCCGTCTGTGACCCTTTCCACTATGTCACCA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt AsnThrLeuHisThrProMetTyrValPheLeuLeuThrLeuAlaValVal}
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seq_documentation_block:
IID AAH32140 standard; DN
AC AAH32140;
XX AAH32140;
XX JOJUL-2001 (first e
XX Human olfactory recep
XX Human; olfactory recep
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XX W0200127158-A2.
XX Homo sapiens.
XX W08-OCT-2000; 2000WO-U
XX O8-OCT-1999; 99US-0
PR 24-FEB-2000; 2000WS-0
XX OB-OCT-1999; 99US-0
PR 24-FEB-2000; 2000WS-0
XX OB-OCT-1999; 99US-0
PR 24-FEB-2000; 2000WS-0
XX New DIGISCENTS.
PA (YEDA) YEDA RES & DE
XX PFI Bellenson J, Smith D
XX WPI; 2001-290713/30.
XX New polynucleotides w
PT sensation for identif
XX New polynucleotides on the sense polynucleotides can the context of antagonists. The meth occ antagonists. The meth occ antagonists and the identific seconts and the identific seconts and the identific seconts and the identific seconts and the identific and edit scents. Libr occ and edit scents individu XX Sequence 948 BP; 240
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                                                                            scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties
                                                                                                                                                                                                                                                                                                                The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; olfactory receptor; OR; primary scent determination; secondary scent determination; polypeptide library; odour receptor; scent profile; scent fingerprint; scent representation; ds.
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                                                            of different individuals.
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24-FEB-2000; 2000US-0184809
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olfactory agonists and antagonists -
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alignment_scores: Quality: Ratio:

699.00 2.937

Length: Gaps:

300

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alignment_block:
US-09-975-308-9 x AAH32140
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13 AATTACACCATGCCAACTGAGTTCCTATTTGGTTGGATTCACAGATTATCT 62
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GCTTCTTTTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGA 362
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|CGGCTATGCAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTA 412
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| CATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGC 612
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                                                                                                              heSerThrCysSerSerHisLeuThrValValThrLeuTyrTyrSerPro 251
||||||||||:::|||||||| :::|||||:::
TCTCCACTTGTGCTTCCCACCTCATAGCAGTCACCTTATTCTATGGAGCG 762
                                                                     ValileTyrThrTyrIleArgProAlaSerSerTyrThrPheGluArgAs 268
                                                                                                                                                                                PLysValValAlaAlaLeuTyrThrLeuValThrProThrLeuAsnProM 285
                                                  CTCCTGTTTATGTACTTACAGCCCACCACTAGCTATTCCCTAGACACTGA 812
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9b_gss:Az913406
9b_gss:Az593814
9b_gss:Az55734
9b_gss:Az55734
9b_est2:BG197640
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gb_htc:AK016560
gb_htc:AK017036
gb_gss:AQ428256
gb_gss:AQ428256
gb_gss:AZ909618
gb_gss:AZ9093339
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Sequence
gb_htc:BC016940
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Query length: 307
Database: EST:*
Database sequences: 13736207
Database length: -1841457050
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-Q=/cgn2_1/USPTO_spoo1/US09975308/runat_24062002_090302_26225/app_query.fasta_1.368
-Q=/cgn2_1/USPTO_spoo1/US09975308/runat_24062002_090302_26225/app_query.fasta_1.368
-DB=EST -QFMT=fastap -SUFFIX=rst -GAPOP=1.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEXI=0.000 -LOOPEXI=0.000 -GAPEXT=0.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=110.000 -YGAPEXT=0.500 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09975308_@CGN1_1_6099
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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AZ909618 RPCI-24-155C12.TV RPCI
BZ93339 RST12467 Athersys RAGE
AZ913406 RPCI-24-156C19.TJ RPCI
AZ913640 RPCI-23-16619.TJ RPCI
AZ9137640 RST17016 Athersys RAGE
AZ055734 RPCI-23-16619.TJ RPCI-
BZ97640 RST17016 MUSCUS 10kb
AZ255734 RPCI-24-331A10.TW RPCI-24-33740.TJ RPCI-24-35740.TJ RPCI-24-35740.TJ RPCI-24-35740.TJ RPCI-24-35740.TJ RPCI-24-35740.TJ RPCI-24-82P2.TJ RPCI-24-3709667 RPCI-23-33618.TW RPCI-24-2767466 ZM0249B07F MOUSCULUS AGULT MA
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gb_gss:BH291047
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 27 Row: 1 Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
DNA Sequencing University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC016940.1 GI:16877381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone has the following Location/Qualifiers
                                                                                                                                                                                                                                                               /clone="IMAGE:4424116"
/tissue_type="Kidney, hypernephroma"
/clone_lib="NIH_MGC_89"
/lab_host="DH10B"
/note="Vector: pCMV-sporT6"
546 c 427 g 578 t
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Metazoa;
Eutheria;
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Similar to olfactory receptor,
ne IMAGE:4424116, mRNA.
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Primates;
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.8e-31
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                                                                                                           41.403
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BH359995 CH230-12616.TJ CH06
A2392036 1M0154P24F Mouse 10
A2972672 2M0246D10R Mouse 10
BH291047 CH230-103B15.TJ CHC
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Mammalia; Eutheria; F
1 (bases 1 to 642)
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2M0241J24R Mouse 10kb plasmid UUGC2M library Mus musculus
clone UUGC2M0241J24 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reil
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0241 row: J column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 642.
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University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ969227.1 GI:13840454
                                                                                                                       Quality:
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                  Ratio:
                                                                                                                                                                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dhares/). The DNA
(http://www.jax.org/resources/documents/dhares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWDA2 (gi|4732114/gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
with adaptors complementary to the insert adaptors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                            purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."

a 166 c 129 g 217 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC2M0241J24"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                      553.00
3.331
77.934
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Rodentia;
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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                         seq_name: gb_gss:BH331857
                                                                                                                                                                                           VERSION
                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                               ThrLeuValThrProThrLeuAsnProMetValTyrSer 288 ::::::||||||||| ||||||||:::::||||::: AGTGTTGTCACACCCATGCTGAATCCTGTAATTTATACG 641
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                                                                                                                                                                                                             CH230-46N15.TV CHORI-230 Segment 1 Rattus norvegicus CH230-40N15, DNA sequence.
                                                                                                                                                                         GSS.
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., Jong,P. and Fraser,C.M.
                                                                                                                                                                                           BH331857.1 GI:17262571
                                                                                                                                                                                                                                                                       BH331857
                                                                           Rattus.
                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                   Rattus norvegicus
                                                                                                                                                       Norway rat.
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Rodentia;
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                                                                                             Euteleostomi;
Murinae;
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BASE COUNT
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                                       GlyAlaGluMetValLeuPheThrThrMetAlaTyrAspArgTyrValAl 122
                                                                                                                          leSerTyrAlaGlyCysMetSerGlnLeuPheLeuPheThrTrpSerLeu 105
                                                                                                                                                                                                                                                                                            MetTyrValPheLeuLeuThrLeuAlaValValAspIleIleCysThrTh
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GGATTGGAAAATGGAATTCTGGTAATGATGGCCTATGATAGGTTTGTGGC
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/fat20, htm). For BAC library availability, please contact Pieter de Jong (pde)ong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tbb/bac_ends/rat/bac_end_intro.html plate: 46 row: N column: 15
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Class: BAC ends.
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2.687
70.000
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
172 c 158 g 313 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="rtaxon:10116"
/clone="CH230-46N15"
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Mus musculus adult male testis cDN
library, clone:4932441H21:similar
                                                                                                                                                                                                                                    Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
                                                    Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
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cDNA, RIKEN full-length enriched
lar to T1 OLFACTORY RECEPTOR, full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted (10-JUL-2000) yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-533-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             with BamHI and XhoI. cDNA of size comprised between 3 and 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
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5 (bases 1 to 3063)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                        BamHI. Host: DH10B.
                           /tissue_type="testis"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
438. _.1388
                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="MGD:MGI:1907565"
/db_xref="taxon:10090"
                                                                                                                                                            /sex="male"
                                                                                                                                                                                              /clone="4932441H21"
                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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                      eCysGlyProAsnThrIleAspHisPhePheCysGluIleProProLeuL 182
                                                                                                                                                                                   TCATGAGTCCAAAGGCCTGCAGGCTCATGGTGGCCATATCATGGATCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                      PheLeuPheThrTrpSerLeuGlyAlaGluMetValLeuPheThrThrMe 115
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VYTMHFPFCMSQEIRHLLCEVPPLLKLACADTSQYELMVYVTGVIFLLLPLSAIITSY
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/db_xref="GI:12855358"
/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/translation="MEPWNSTLESGFILVGILDGSGSPELLCATVTTLYMLALISNGL/translation="MEPWNSTLERGCSLIDLFTSVVTPNTVVDFILADNTISFEGCALQLF"
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                                                                                                                                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNas to prepare full-length cDNa libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Hazada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Please visit our web site (http://genome.gsc.riken.go.jp/) for
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we RIKEN Genome Exploration Research Group Phase II Team and
   355
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337 c 304 g 398 t
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                                                                                                                                                                                                                                                                                                                                                                                                                        TCATGAGTCCAAAGGCCTGCAGGCTCATGGTGGCCATATCATGGATCCTA 784
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                                                                                                  rGlyPheIleIleValAlaIleLeuArgIleArgThrValGluGlyLysA 232
                                                                                                                                                                      AlaAspIleThrLeuAlaIleGlyAspPheIleLeuThrCysIleSerTy 215
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                                                                                                                                                                                                                                                                                TTGCATGTCCCAGGAAATCAGACACCTGCTCTGTGAGGTTCCTCCATTGT
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                                                                                                                                                                                                                                                                                                                                                     GCATCTCTTAGTGCCCTAGGTCACACAGTGTACACAATGCACTTCCCTTT
AGAAAGCCCTTGTCACCTGTTCCTCCCACTTGACTGTGGGTTGGGATGTTC
                                                                    CTCACTAATTCTATTCACTGTGCTGCACATGCCTTCAAATGAGGGCAGGA
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LOCUS AQ428256
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                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Other_GSSs: CITBI-E1-2578F11.TR
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 2
                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: M13-21 Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301 838 0200 Fax: 301 838 0208
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Use of BAC End Sequences
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Mamumalia; Eutheria; Primates; Catarrhini; Hominidae
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/note="Vector: pBeloBAC11;
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/db_xref="taxon:9606"
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LOCUS AZ909618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                             Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                  Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 222 row: G column: 18
                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the mouse BAC library RPCI-24. For I library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorg Russell, D., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 797)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA sequence.
                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:1090"
/clone="RPCI-24-222G18"
/clone_lib="RPCI-24"
/cell_type="Spleen/Brain" /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pleter de Jong. The library was cloned in the pTARBAC1 cloning vector at the
                                                                                       /sex-"Male"
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences from Library
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alignment_block:
US-09-975-308-9 x AZ909618/rev
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ORIGIN
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Percent Similarity:
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                                                             sLeuThrValValThrLeuTyrTyrSerProValIleTyrThrTyrIleA 258
                                                                                                ValMet.....ValTyrValAlaAspIleThrLeuAlaIleGlyAspPh
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                                                                                                                                                                  TCTCCTGCATCCTCCTCATATGCCTTCATTGTGGTTACCATCTTGAAG
                                                                                                                                                                                              elleLeu.ThrCyslleSerTyrGlyPhellelleValAlalleLeuArg
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rgProAlaSerSerTyrThrPheGluArgAspLysValValAlaAlaLeu
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                                 CCTCACAGTGGTGGTTGTACATTATGGCTTTGCTTCTGTCATTTACCTCA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uAsnThrIleSerTyrAlaGlyCysMetSerGlnLeuPheLeuPheThr. 102
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alignment_scores:
    Quality:
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90 TCTCCTCTTGTGTTCTTCCTCAGCATGTACCTGGCCACTGTCCTGGGGA
                                     22 yIleIlePheLeuPhePheLeuIleValTyrLeuValAlaPheLeuGlyA 39
                                                                                       40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
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                                                                                                                 6 ValThrGluPheIleIleLeuGlyLeuThrLysLysProGluLeuGlnGl 22
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                                                                                GTCTCCGAGTTCCTCCTCTTGGGACTCTCCAGGCAGCCCCAGCAGCAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Calin,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith, E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression
activation of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3201 Carnegie Ave, Cleveland,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21227151
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1 (bases 1 to 762)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RST12467 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence BG193339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG193339.1 GI:13715026
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                                                                                                                                                                                                                                                                                                                                                                                                                                              152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Libraries using Random Activation of Gene Expression, Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

253 c 156 g 201 t
                                                                                                                                                                                                                                                                                     514.00
2.872
73.663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                             from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_gss:AZ913406
                                         Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Contact: Shaying Zhao
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 794)
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TGACCATCATGAGCAGAGGGCGTTGCATTGGGTTAATAGTGGCCTCCTGG
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                                                                             rThrMetAlaTyrAspArgTyrValAlaIleCysPheProLeuHisTyrS 130
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                                                                                                                           CAGATGTTCTTCCACCTTATTGGGGGAGTGGATGTGTTTTCTCTGTC
                                                                                                                                                         GlnLeuPheLeuPheThrTrpSerLeuGlyAlaGluMetValLeuPheTh 113
                                                                                                                                                                                          TAGACCTTCTCAGACAGAAAGACCATCTCTTTCAATGGCTGTCTCACT
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The Institute for Genomic Researc
9712 Medical Center Dr., Rockvill
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2.583
74.157
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/clone="RPCI-24-165C12"
/clone_lib="RPCI-24"
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                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0405 row: K column: 03
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
University of Utah Genome
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ593814 580 bp DNA linear GSS 13 1M0405K03R Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0405K03 R, DNA sequence.
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308,
                                                                                                                         quality sequence stop: 580.
Location/Qualifiers
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801 585 7177
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                             /clone="UUGC1M0405K03"
                                                 /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                      /organism="Mus
                                                                                                                                                                                                                                                                                                                                                                                                                        scaffolding with paired end reads from 10kb
                                                                                    musculus"
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alignment_block:
US-09-975-308-9 x AZ593814
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                251 TGCTATCCTATGGCTGCATCATTGCCAGCATCCTGCGCATGCGTTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 lMetAlaIleAlaValThrAsnSerTrpValHisThrAlaLeuIleMetA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 ATGGTCCATCAGTGCTGTGAATGCATCTGTGCACACTGGCCTGATGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TACAGCTCTAGGATGAGCCCACAGATGTGTGGGGGCCCTGGCCATGGGTGT
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ThrProThrLeuAsnProMetValTyrSerPheGlnAsnArgGluMetGl
                                                                                                          erTyrThrPheGluArgAspLysValValAlaAlaLeuTyrThrLeuVal 278
                                                                                                                                                                     CTCTGTGTACTACTCATCTGTGTTCTGTGCCTATGTCAGCCCTGCTTCCA
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                                                     GCTACAGTCCAGAAAGAAAGTTACCTCAGTGTTATACTCGATCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli xIIJO-Gold (Stratagene) cells and selected for amplicible resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
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/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 c
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alignment_block:
US-09-975-308-9 x AZ255734
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ORIGIN
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LOCUS AZ255734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ### AGCCCAACCCTCATCTATACACTGAGGAACAAGGATGTCAA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nAlaGlyIleArgLysValPheAlaPheLeuLysHis
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                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones availability, please contact Pieter de Jong

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 166 row: I column: 9
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-16619.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shao, Levins, M., Mcgann, S., Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ255734.1 GI:9458784
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                                                                                                                             Ratio:
ф:
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                                                                                                                                                                                                                                                              167
AZ255734
                                                                                                                                                                                                                                                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                      504.00
2.816
74.895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="RPCI-23-16619"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
from:
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genomic clone
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KEYWORDS
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ORGANISM
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LOCUS BG197640
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    REFERENCE
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                                                                                                                                                                                                                                                                                                                                      256 yrIleArgProAlaSer 261
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                                                                                                                                                                                                                                                                                                                                                                                  TTCCCACATAATTGCTGGTTCTCTCTTTTTGCATCAGGTGCATTTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTTCTGTGACATCCTCCCTGTGATGCAGCTCTCCTGCACCAGCACCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysPheProLeuHisTyrSerThrIleMetAsnHisHisMetCysValAl 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGAGTGTTATGTGTAATGTCAATGGCCTATGATCGCTATGTAGCCATC
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Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
1 (bases 1 to 796)
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BG197640
BG197640.1 GI:13719455
                                                                                     human.
                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCTCTTCCTGCTGCTGATGTACCTGTTCACGCTGCTGGGCA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yIleIlePheLeuPhePheLeuIleValTyrLeuValAlaPheLeuGlyA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTCTGAATTCATCCTCGTCTGCCTTCTCTGCCTTCCCCCACCTCCAACT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValThrGluPheIleIleLeuGlyLeuThrLysLysProGluLeuGlnGl 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snMetLeuIleIleIleAlaLysIleTyrSer...AsnThrLeuHisThr 54
                                       rValAlaIleCysPheProLeuHisTyrSerThrIleMetAsnHisHisM 137
                                                                                     LeuGly...AlaGluMetValLeuPheThrThrMetAlaTyrAspArgTy 120
                                                                                                                                                                           CCATCGCCTTCCTGGCCTGTGCCAGTCAGATGTTC...TTCTCCTTCAGC
                                                                                                                                                                                                                hrIleSerTyrAlaGlyCysMetSerGlnLeuPheLeuPheThrTrpSer 104
                                                                                                                                                                                                                                                                   CGTGGCCATCATCCCGCGCATGCTGGCCGACCTGCTGTCCACCCAGCGCT
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                                                                                                                                                                                                                                                                                                                                                                                         ProMetTyrValPheLeuLeuThrLeuAlaValValAspIleIleCysTh 71
                                                                                                                                                                                                                                                                                                                                                                                                                                          AC...CTGTTCATCATGGCCACCGTCTGGAGCGAGCGCAGCCTCCACACG
  CGTGGCCATCTGCCCACCCCTGCGCTACAACGAGCTCATGAGCCCACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3201 Carnegie Ave,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,J., Danzig,J. and Ducar,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"See 'Creation of Genome-wide Protein Expression /Inbraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

a 271 c 189 g 220 t 1 others
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/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
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2.595
78.543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eValAlaIleLeuArgIleArgThrValGluGlyLysArgLysAlaPheS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 unn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reil,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern, and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ607393.1 GI:11729583 GSS.
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1 (bases 1 to 740)
                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: N column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                  University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome
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                                                                                                                                                                                         Class: plasmid ends
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Location/Qualifiers
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801 585 7177
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                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
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                                    /clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant,
/note="Vector: PWD42nv; Purified genomic DNA from
                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                            scaffolding with paired
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alignment_block:
US-09-975-308-9 x AZ607393/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  739 TTCACTATGTTTCTAGTTGTTTATCTTACTAATCTGCTGACAAATCTTGG 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 rAlaGlyCysMetSerGlnLeuPheLeuPheThrTrpSerLeuGlyAlaG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 alPheLeuLeuThrLeuAlaValValAspIleIleCysThrThrSerIle 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 IleProLysMetLeuGlyThrMetLeuThrSerGluAsnThrIleSerTy 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 uIleIleIleAlaLysIleTyrSerAsnThrLeuHisThrProMetTyrV 58
                                                                                                                                                                                                                                                                                                                                                                   uLeuSerMetValMetAlaIleAlaValThrAsnSerTrpValHisThrA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PheProLeuHisTyrSerThrIleMetAsnHisHisMetCysValAlaLe 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTGGCTGTGCTATGCAGTTCTTCACTTTCTGTATTTTTATAGATGCTG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCCTAAGATGCTTGTAGACCTACTGTCTAAGAATACATCTATTCCTTT
eAsnGluValMetValTyrValAlaAspIleThrLeuAlaIleGlyAspP 208
                                                                                                                                                                                                                                          laLeuIleMetArgLeuThrPheCysGlyProAsnThrIleAspHisPhe 174
                                                                                           PheCysGluIleProProLeuLeuAlaLeuSerCysSerProValArgIl 191
                                                                                                                                                                                 CATTGACATTCCACTTATGTTTCTGTGGGTCGAATGAGATTAATCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                               AACCCCCTTTTGTATGCAGTAGACATGTCCAGGAAAGTGTGCCTTCCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheLeuPhePheLeuIleValTyrLeuValAlaPheLeuGlyAsnMetLe 41
                                                                                                                                                                                                                                                                                                       AGTGTGTGCTGCCAGTGATGGCATTTGATCGATATAAGGCCATTAGT 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGACTGCTGTTGCAATTTTTCAAGGAACTATGCTCTTCATGTATTC.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCAGTTCTGCTGCGGAGGTTAAAAGCTTTCTCTACCTGTACATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCAGGAGTTCTTATCTCCTACTGTTACATCATCTCATCAGCTTCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleArgThrValGluGlyLysArgLysAlaPheSerThrCysSerSerHi 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   helleLeuThrCyslleSerTyrGlyPhelleIleValAlalleLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_gss:AZ353949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Errr
Plate: 0093 row: J column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 676)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ353949 676 bp DNA linear GSS 0: 1M0093J01F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0093J01 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.10.5 kb range using preparative agarose gel
                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                       musculus C57BL/6J (male) was obtained Laboratory Mouse DNA Resource
                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC1M0093J01"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aGlyCysMetSerGlnLeuPheLeuPheThrTrpSerLeuGlyAlaGluM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProLysMetLeuGlyThrMetLeuThrSerGluAsnThrIleSerTyrAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        etValLeuPheThrThrMetAlaTyrAspArgTyrValAlaIleCysPhe 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euIleMetArgLeuThrPheCysGlyProAsnThrIleAspHisPhePhe 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uSermetValMetAlaIleAlaValThrAsnSerTrpValHisThrAlaL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCTCCACTATATGACTATCATGGACCGGGAGAGATGCAATAAGATGTT 216
TGCTGTTGTCATCATTTTTTTTGGCCCCTGTACTTTTATGTATATGCGGC
                                                                                                                                                                  uThrValValThrLeuTyrTyrSerProValIleTyrThrTyrIleArgp 259
                                                                                                                                                                                                                      CAGTCATCCGAAGGCAGACGCAAAGCTCTCTCCACTTGTGGATCTCACAT
                                                                                                                                                                                                                                      ArgThrValGluGlyLysArgLysAlaPheSerThrCysSerSerHisLe 242
                                                                                                                                                                                                                                                                                            leLeuThrCysIleSerTyrGlyPheIleIleValAlaIleLeuArgIle
                                                                                                                                                                                                                                                                                                                                                                  TGGTGTTGTGACAGCCAACAGTGGCACCATTGCATTGGGAAGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                   nGluValMetValTyrValAlaAspIleThrLeuAlaIleGlyAspPheI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGATGTACATCCTGTACTGAAACTTGCCTGCACCGACACTTACATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysGluIleProProLeuLeuAlaLeuSerCysSerProValArgIleAs 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTGGTCCAGCTCCCATTTTGTGGACCAAATGAGATTGATCACTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCGGAACATGGATCAGTGGCTTCTTACATTCTATTATCCAAGTGGCTC 266
                                ThrLeuValThrProThrLeuAsnProMetValTyrSerPheGlnAsnAr 292
                                                                     CTGACACT....ACCTTCTCTGAGGACAAGATGGTAGCTATATTTTAC
                                                                                                      roAlaSerSerTyrThrPheGluArgAspLysValValAlaAlaLeuTyr 275
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RPCI-24-331A10, DNA sequence.
BH069789
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Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 331 row: A column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao, S., Nierman, W., Malek, J., Shatsman, S., Ak
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS
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1 (bases 1 to 698)
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Other_GSSs: RPCI-24-331A10.TJB
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DNA."
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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/clone="RPCI-24-331A10"
/clone_lib="RPCI-24"
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/strain="C57BL/6J"
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STIC-Biotech/ChemLib

To: Subject:

From: Sent:

Li, Ruixiang Thursday, June 20, 2002 9:56 AM STIC-Biotech/ChemLib Sequence search of Application NO: 09/975,308

Please do a standard search on SEQ ID NOS: 8 and 9 against both the commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li GAU 1646 CM1 10E18 Mail Box 10C01 306-0282

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

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Location:
Date Picked Up:
Date Completed 26/10
Searcher Prep/Review:
Clerical:
Online times

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